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(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen *et al.*, *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.
10
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of
10 polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with
polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + y^4 + z^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30
$$\text{cum } p(\text{ID}) = p(\text{ID}_1)p(\text{ID}_2)p(\text{ID}_3)\dots p(\text{ID}_n)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a
5 Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next
10 generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,
5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1.

The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different reference sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C T	---			TGTGAAACTCCACTTGAAGCCAAAGAAACATTCACACTTAAACACATGCCAGTTGGGAAGGTC GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAACACAGTTGAAGGAAAGACATTGGAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTCTTTC/TAAGTTTAATGCTGTCTCTGTCAG
WI-10744	61	G C	---			AAGCCATTGACGTAAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAGCCCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATCTCTGAATT AAATGAGTTAAGTTTCAGGCACTCA
WI-9975	126	C T	---			GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAAGTCAGGTGCAAGGGAGGTAGAACA TTACAGTAACATATGTCAAATCTTTTGTATATTAGTATTATCTGCCAATGCCCTAGAATA[C/T]AGTG GGTCCCTAATAGTTATTAGTTCCTTTTCTCCCTCTCTCAITCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTATGATCAATTTGATCTTACTGAA
WI-8010	247	G T	---			GCTAGGTTTGTCTGTGGCTGCTTCCTCAGTACACTTGAGATGACTTGATTACAGTAATCCCTATGT GATGTAACTAGTCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCCCTCTCCAGTTTCATCCTGTATTAAATTTCTCCCATATTAAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAAGAGATCCCAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G C	---			GCCGGCCTATCTTTAATTTAACTTGATCTTTGGGTCTCCATCCTAGGATTCGCCCTTATAAT CTTTGTCTGTCTGTA[G/C]ATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGTCTCTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTTCTACTTA TCTGACTCTATAACAACCTCCACAGAA
WI-5222	52	G C	---			GCCGGCCTATCTTTAATTTAACTTGATCTTTGGGTCTCCATCCTA[G/C]GATTCTGCCCTAT AATCTTTGTCTGTCTGATGATTAACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGTCTCTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTTCTACTTA TCTGACTCTATAACAACCTCCACAGAA
WI-8007	242	C A	---			TATGCATCTCCACAAAAGCGATATAATTTAAAAGTTTTTTTCATTAGAAATAAATGTATAAAAAATA ATATGTTATTATAGGCATTTTACTAATCTAGTCCCTCTTGGAAAGGAACACCCCAACCAATACTT ATAAAGTACATGTAAATTTATAGTAACATAATTTACTATATACATATGGAAAAAATCATATTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[C/A]AGCTGCTG
WI-9823	97	C T	---			TCAGTTGCAAAAAATTGCTGCCATAAACATGCTTTTGCCTTATCTCTGTGCATATGTATGTGTTTGTAG TCTATATTACACACATAGTGAATTTTC/TTGGGGCATGGGAAATACATCTTTTATGAGACATTTGA ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACATGTATAAGAAATTOOCTTTGTTTAC ATGCTTCCCAATCTGATTTGTAIGACTATTGATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	---	TCCTACATTCATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCTGGAATCCCTTCCT ACTTGTCTCATGTACAAATTTCTGCTCGTCTTCA/TJGGGACGCTTCAAGCCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCAGGGACCCCTTATAGGCCTCTG TCITTAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGTCTCTC
WI-9651	139 T C ---	---	---	TCCTACATTCATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCTGGAATCCCTTCCT ACTTGTCTCATGTACAAATTTCTGCTCGTCTTCAAGGGCAGCTTCAAGCCCTCCCTTTAGACACCT CT/JACAGGTACAGCCGACCATGCCCTACCTCCATGCCACTGCCAGGGACCCCTTATAGGCCTCTGT CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGTCTCTC
WI-7676b	309 A C ---	---	---	GTGACCTCCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGTAGATGGGAGGCTGTGTGAAGGG GCCGCTCTCTTGGTGCTGCTGGTTCAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGTGC TCCCCCGTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	---	GTGACCTCCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGTAGATGGGAGGCTGTGTGAAGGG GC/JGGCTCTCTTGGTGCTGCTGGTTCAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	---	CATTATCTTGCTTGGTGCTGTTCAATCCTTCCCTCTCCCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGATTTGAATAATTTTGTG/JGTGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTCTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACACCTTATAGATATTAATATCTTT
WI-9986	42 T C ---	---	---	TTGGTGTGAACCTCAGAAATATAGGAAATTAAGACAATTTGAAT/A,CJGTACCCACAGGAACAAGAG CCCTGCACCTTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGTAGTACTACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGCACCTCCCACTCTCATCGCCCAAGTGGAGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTATTT CAGGGCTTTGCATGCGCTCTATTCCTCTGCTCTGCTC/JCJCCACCTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAACAAGCTCAITTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ---	---	---	ATAAACCTTGTGTATGATACCCCAACTCAATATATCAACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAATCCTAAACATCAAACTTTTCATCCATAAAATGTCAGCATTT /CJATTAATAAACAAATAACTTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAATAAAG GCATTTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	TCCTATTGCAATTCACAGTAGCCCCCATGAAGTAGGTATACCAGCCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTCTCAGGTTTTCTTAATAAGCAAAGACCTGCA/AC JCCCTGGCTTCCTGACTCCAAAGCTTATCCCTCTCATGCTGTTGCTGCAGCCAGGACCCCATGGGCA GAAAGCCCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACCTTTGGAGATTCATTTCTTGAGTGGCACTGCAT GCTCATTCAAGTGAAGAACCTTGTTGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAACCATCACCTGGTTTGCATTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACACAGAATCATCAAGCAC/AT/ATCTGTGTTTGAGATAAATGATGCTGAGTCACCTATG TAAGAAGTAAGTCTGAAATAGTAGGATAGTATATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTCACTTCTATGGAAGTCTCCGTACTGTAATTTTCACTTCTATGGAAGTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAATAAGAACACATTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTATAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAAGTAGCAATGGGAATGAAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAAGAACTTGAT
WI-4719b	107 T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT AT[G/A]CTGACGCCATGGGTGTTTCAATAGTGACTTGAAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATTCGTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT AT[G/A]CTGACGCCATGGGTGTTTCAATAGTGACTTGAAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATTCGTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCATTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTCTGTGAGAGGGAGGGCCAGACAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGACCCAGGGTTCCAACTTT
WI-9484	178 G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCATTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTCTGTGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGACCCAGGGTTCCAACTTT

WI-7330	207	C T ---	---	AGGATGAAGGAGACACGGGAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATCTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAAG TGAGAG[C/J]TGAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211	G A ---	---	TAAAAACAGTTCAGGTTGGTGAAGCAGAAAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACIT GCACAAATTAATCTCTTGGCATCATACAACTGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACTCATGGAAGGAGCTAGAGTCCATCAGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCACATGCCCACTT
WI-7166	59	C T ---	---	TCTCTAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/J]GGAT CATCAACAAGATTCTTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCTTGAATAATTCGTG ATTTCAAGCAGCATCTTCTGGTTAAACTTGTGCTGTGAACAAATGTGCAAAAGAGTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C ---	---	GCTTCTCCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTAGCC CCACCTCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT[C/J]TGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTGCAAGGGGCCAACTTCCCTGGAGCTC
WI-7259	188	G T ---	---	GCTTCTCCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACA[G/C, I]TGGGGGAGCA GAGCAGCAGGTGGACAGGTGTTGCAAGGGGCCAACTTCCCTGGAGC
WI-7322	275	A G ---	---	GTACTTTAGGCTGTGAGGTTGGGCAATTTAGTGTGACCTTGCACCAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCTATATG GCCATAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCTTTGACCAGAGAAAGCACTC TGGTCTCTATCCCTTGTACATAGAGATTGTGATGGGCCCTCTGGCTG
WI-7685	46	T C ---	---	TCAGTTCTAGTCTCTCTGGGCCACACAGAAACTCTTTTGGGCT[C/J]TTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGACCAAGGCTTGGAGCTGAGCCTCTACCTGTACTCTCCGAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCTCCCTCTGCGGACTC CTGGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTCTGTCTC
WI-563	87	G A ---	---	TGTGACCAATTGTTATTTAGAGGTTTAAACAATGGCCTGACTATCACCTGATGGTCGCCAATTC CTGGGGAGGCGCTCCCTT[G/A]CCCTGATCATGTCTACCTAACTACTCTAACAACTACTCTCC TGTGGTATGGGATCCTAAGCCAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAAAATTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191	C A ---			GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCACAAATGATCCTCT GTTGCTGCACCTGTCATTACTGTTGTATGGATTTATAATATTGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	A G ---			GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTT[A/G]TCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACCTGTCATTACTGTTGTATGGATTTATAATATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	A G ---			GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAG GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGCTGTGTCACAAATGATCCT TCTGTTGCTGCACCTGTCATTACTGTTGTATGGATTTATAATATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	C T ---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAATTAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-10870	103	G A ---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAAGTGGGACCTACTTAGA[G/A]CAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAATTAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-7719b	281	T C ---			AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCAATTGGCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCTACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---			AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCAATTGGCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[G/J]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCTACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---			GCCTTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTTCTTTTGTTA TGCCATTGAGGGATTGATGTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTCAGG TTAACAGCCACCATTTGTAAACACITTTGT

WI-10673	94 C G ---	---	TCCCTTTATGCACCCAAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGCTGGCACTCATGGAGGGGG[C/G]TGAGGTTGGAATATGCAATGCTGCTCCGGCCACACA TCCTGCTGGCCCCCTACCTGCCCCAAATTCATCTCTGCAATTAATCTGCTTATTGTTTCATCCTG GAGAAATTGAAGGGAGGTCAAGTTGTTGTCAATGATTGTCAGAGAACCT
WI-7842	57 T C ---	---	CACAGCCATGCCCTTGAGGAGCGGCCACCAGATGCTGAATCCCTATCCCATCTG[C/G]TATGAG TCCCATTTGCCCTTGCAATTAGCATTTCTGCTCCCCCAAAAAGAAATGCTATGAAGCTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACITTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	CTGCCCTCATACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCCAGCTGTACCAGCCGGGCGAGGTGCAGCCCTTCTCTCC TGCTCTG[C/A/C]TCTGACTCTCTTTTGAGGTCCCTGTATGTTCTACTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCT CAGGTCTGGTAACTCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATCCACTAAGA CTCCTCTAACCCAGAGATTTTAACCT
WI-4767	50 A G ---	---	TTTCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA[C/A]GATTCATAAAGAGTT CCTCAGGTCTGGTAACTCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGAGGGTATG TTTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTCTAACCCAGAGATTTTAACCT
WI-7718f	222 C T ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAAGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718b	248 A G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAAGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718a	42 A T ---	C		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAAGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7227d	99 G C ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTAGCJAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACAGTG TTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACTGGCTTC TTCCGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---			CCACAATGCCCTCCACGATGTCAAGGACTCCTGTCTGCTCGAGGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGATCTTCATCGAACAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAAGGACATGTGCTATTGAATGAGCCCAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA/CJATGATCTTGAGATTTC

WI-7310a	64	T A ---	---	CCACAATGCCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGGAGACAAGGAACQTTA JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAACAACTGATCGGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAAGTGGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162	A G ---	---	CCAGCAACACCTACACCCCTTGTCACCTGCCCTGGACTCCTATGATGGCCTGTC/GTGGTTGATAATAACA GATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGGATGATTGCAATGGAGGGCAAAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG/G/GTGTGATGAAGGTGATGTTGGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTCACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51	C G ---	---	CCAGCAACACCTACACCCCTTGTCACCTGCCCTGGGACTCCTATGATGGCCTGTC/GTGGTTGATAATAA TCAGATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGGATGATTGCAATGGAGGGCAAAATGCG GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTCACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213	C T ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCTAACC AGCCCTGCAAGTTTCCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCCTGCTATGGTGAGATC AGATGTGGCCAAAGGAAGGAGCTCTGGTCCAGAGAAATTTGCACAAAGTTCCTCTGTACAGAGACA AAAGGCCCTC/TJGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54	C G ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGGTCCAGAGAAATTTGCACAAAGTTCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53	C G ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCT ACCAGCCCTGCAAGTTTCCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGGTCCAGAGAAATTTGCACAAAGTTCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93	G A ---	---	AAATTGCTCTATTGGACCCCTCATATTAAATAAGAGCAATGAGAGCGAGGAAAAATTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92	G A ---	---	AAATTGCTCTATTGGACCCCTCATATTAAATAAGAGCAATGAGAGCGAGGAAAAATTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC

WI-1795b	130	T C ---	---	---	GAAGCAACCAAGATATCTTTATCCCATCTAGATTATGCTGGGTTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCCTTGCGAGAAAGAAAGT/CJC GTCTACCATTTTACCAGAAATTCGTAGTACAATTTAAGTATCTCTTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47	T C ---	---	---	GAAGCAACCAAGATATCTTTATCCCATCTAGATTATGCTGGGTT/CJCTTCCAGACTCCTACGA TTAAATTGATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCCTTGCGAGAAAGAAAGTC GTCTACCATTTTACCAGAAATTCGTAGTACAATTTAAGTATCTCTTGTTATCTCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136	G A ---	---	---	CACACAATTTGCAACACTTCAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACAATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616c	136	G A ---	---	---	CACACAATTTGCAACACTTCAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACAATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616b	141	C T ---	---	---	CACACAATTTGCAACACTTCAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACAATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616a	116	G C ---	---	---	CACACAATTTGCAACACTTCAAAGTGAACGCCCGACATCATAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAGCGTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACAATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCCCTCTGAGACTCCC ATGGATCATCTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-1126c	52	G A ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATATAATAATAA AAACCCGTGAAGTCTGCTTGCAATTTCAAGATTCATATATATCCAGATTGTTTCCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATATTTAATTTTCAAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAAAATCCAGCTGAACTTTTTTTGGACTTGCTTTTATTTCTT
WI-1126b	230	T C ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATATAATAATAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTCATATATATCCAGATTGTTTCCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATATTTAATTTTCAAGTTTCTCAAAAGGAATATGAAATTGTT AAAATGCAAAATCCAGCTGAACTTTTTTTGGACTTGCTTTTATTTCTT

WI-1126a	97 T C ---	---	---	CTCTATTCTCTGGGCACTGCCTTCTTTGGGGCAAACTCCAGTATCACTGATACTAATAATAAA CCCTGTAGTCTGCTTGCATTTCAAGATTC/CAATATATATCCAGATTGTTTCCAGCAAGAAAA ATTTATTTCTCAAGATATAAAAAATAATATTAATTCAGTTTCCCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTGGACTTGCTTTATTTCTT
WI-11183c	124 C T ---	---	---	TAGTGCTAAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---	---	---	TAGTGCTAAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---	---	---	TAGTGCTAAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCTTGTCACATAACATA TTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---	---	---	GCTTGGTTGCTTAGCTTATTGCTCAGCTTGAGTTCTCCCTTCTGCGTGGCCCTTTTGATTTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCCCTATCTGGAGCGCTCTCCCTTGACTTTCTCCTG TTCACCAACCTCTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGIGCCCTTTCC
WI-10770a	49 G T ---	---	---	GCTTGGTTGCTTAGCTTATTGCTCAGCTTGAGTTCTCCCTTCTTG/TCCTGGCCCTTTTGATTT TCACCCATACCTCTATGCCCTGCTCAGACCATTTCCCTATCTGGAGCGCTCTCCCTTGACTTTCTC CTGTTCCACCAACCTCTTTTATTCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGIGCCCTTTCC
WI-9667b	82 C T ---	---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTTGATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATCT
WI-9667a	68 G C ---	---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTTGATCATG GCTTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATCT

WI-10400d	189 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTAAGATGGTTTAGCACACATGTAGCACATTTACTAACACAATATTTTATCTAAATTTT TCCTTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTC[A/G]TGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATTATCAAGGGGTTAATGCATTATG
WI-10400c	166 A C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTAAGATGGTTTAGCACACATGTAGCACATTTACTAACACAATATTTTATCTAAATTTT TCCTTCCCTTACCTTACTCCTCCCAACCA[A/C]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATTATCAAGGGGTTAATGCATTATG
WI-10400b	165 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTAAGATGGTTTAGCACACATGTAGCACATTTACTAACACAATATTTTATCTAAATTTT TCCTTCCCTTACCTTACTCCTCCCAACCA[A/G]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATTATCAAGGGGTTAATGCATTATG
WI-10400a	46 T C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTA[A/T/C]TGCAATTTTCAGACATCT GCTGGTTAACTGTTAAGATGGTTTAGCACACATGTAGCACATTTACTAACACAATATTTTATCTA ATTTTCTTCCCTTACCTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAAATTATCAAGGGGTTAATGCATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCA[C/T]TTAGAAAGGGCAITTCAGCACATTTCAATGAGGCTTCATATCTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCATGTAGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAACTAAGGCCAAACCATGA[A/C]TJGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACCTTAGAAAGGGCAITTCAGCACATTTCAATGAGGCTTCATATCTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCATGTAGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCCTCCTCCAGGAATGCTGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCCTCCTCCAGGAATGCTGGCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTGAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31	G A ---	---	CGAGCTGGGATAAAGCAAGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTGTGGTGTCCCAATGAATACTAGATGCTGGGCTGTCTCCCTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAAGAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTCTGA
WI-3429b	64	G T ---	---	ATACGCTTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCGGCTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T ---	---	ATACGCTTTCTGTCTGCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCGGCTCCACAC[CT/AG] CCCTCAGCCCCCTCAGCTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAAGAGTGAGTGACGGTGACCT GTGAGCCCCATTCTT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786b	111	A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786a	106	A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6711b	226	G T ---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAATTGAATAAGTATGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTGAAAT TTCATATACCTCCATTATTAATTCATATACATCATTCAGAGAAAAGACAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGTATCTCTAAA
WI-6711a	36	T C ---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAAT[CT/G]TAATAAGTATTTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTCT GAATTTTCATATACCTCCATTATTAATTCATATACATCATTCAGAGAAAAGACAACGGTGCCAACTG GGTTGGTGGTGCCTGCACACCCACAGTGGCAACTAAGTGTATCTCTAAA

WI-10613b	172 A C ---	---	ATTGATGCCAAAATCAATAACCTGCATTCCTAGAACATACAGTGAATAGAAATTTGAGCCATA TGTTGAAAAATTTAGAAAGTATTATCTCTATATATATACTACGTTTAAATCAATGAATGTGATTT TTTGCAACTTTTGACAAGGCCAGGCAATTTTATTG/C/GCCCTAGGAGGTTACTATAATTTAGA AAGGCTTTAOCCTTCACCTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	ATTGTATGCCAAAATCATAATACCTGCAATCTAGAAACATACA/GA/JTGTAAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATCTCTATATATATACTACGTTTAAATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCCTTCACCTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA/J TJGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCTTGAAGC ACATCCCTCTCTG/JA/JCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTC/JG/JAAGATCTGTGCTTTCCAAAGTGACTACCTTGA AGCACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCC/T/A/AAAGACAGCCATTTTAAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-10681a	41 A T ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTG/JT/JCTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCTAAAGACAGCCATTTTAAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-7222c	126 G T ---	---	GCCTCTCCTCAACTGCTCGACCCCAAGGCTAGGAAAGGCTGCTTGAAGTACTGTGTCGCCCTT AGACTCCCTAAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG/J/JAATAA AGGAGGGGAATTCCTTTGAACAAGAAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTTCAAGACTCGAATTCATTTT

WI-7222b	255 G A ---	---	---	GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTAGGTGTCAACCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126 G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTAGGTGTCAACCTGTTCTCAAGTTGGGGATGGG[G/T]AATAA AGGAGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41 C A ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTT[C/A]TTATCTCCTCCAGTTCAAAATG CTTGCACTTTTAAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCA CAATCTTCTTTGTAGTTTTCAGCCTTTTCCGGAAATCGGCTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCAATACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054c	237 G T ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTAAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCACAA TCCTTTGTAGTTTTCAGCCTTTTCCGGAAATCGGCTAGTTTGGCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054b	148 T C ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTAAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAG[C/G]A CAATCTTCTTTGTAGTTTTCAGCCTTTTCCGGAAATCGGCTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCAATACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054a	131 C G ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTTCTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTAAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAG[C/G]A CAATCTTCTTTGTAGTTTTCAGCCTTTTCCGGAAATCGGCTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCAATACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-10854b	152 G T ---	---	---	TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAAGCAGTAGTTAACGCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA[G/T]GGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTTG TG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102 C T ---	---	---	TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTTG TG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ---	---	---	AATTTATATGTAAGGGTTAGCAAACTATGCCCCACAGGCCCATTTAGCCATGCCATTTTGTG TGCTGATGGCTGTTTGGTGTTCACGAGTTGAGCCATTGTGACAGAGGCTGTTATGAGCCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGAAAGTTGCTGATCTAGATATTTAAAG GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ---	---	---	AATTTATATGTAAGGGTTAGCAAACTATGCCCCACAGGCCCATTTAGCCATGCCATTTTGTG TGCTGATGGCTGTTTGGTGTTCACGAGTTGAGCCATTGTGACAGAGGCTGTTATGAGCCCTT AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGAAAGTTGCTGATCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G TGGGTTTT	TTGTTTGTGT	TGACATTATAT AAACGTAATAA GAAAATGT	CGGACACGTGATATACAAATACAGATCGTATGGGTTTGTGTGTGGGTTTTTTTTTGTGTTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G AG	AACTGCAAAT AGGAAACCAG	CCACCTGGGGC TOOC	TTCAAGTAACGTCAAATAGGAACCAGAGAG/GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCCCTACACCCCTTAT
WI-8170b	259	G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACATTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAACAAACATAACACAAGA
WI-8170a	204	T A ---	CCTTTATTAAA ATTGTTTTCTT	---	GCACCTCTCTCTGAGCAACAGGTACACATTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAGTGCAATCCTATCAATCAGAA A/T/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAACAAACATAACAC
WI-8172	136	C G GACA	TGAAATAAAA ACAAATTTCTGT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCTTAAAGTCACTCTCCAAATCTCCAGGTCAATGGTGAAGATCACTGTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTTAAATGTTTCTTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56	G A TGC	---	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTACATGAAATAAAAACAAATTTCTGTTGC/GAGCAGGTT TGATTTCAACACAGTTGAATCTGTAAAACCAAGCTGTTCTGATGCAGGACAAATATOCACAAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCCTTATGGGATTGCAAGCGTTACAGGTTAAAGACAAAACCCCAAGCATGGGATTTGCCGGAAAT ATTAGCGTTAAAGGAG/C/TTGAGTTGAGTCAACACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTACAGACAGGGAAGAGGTAGTGGAG/GAGATGGTCAGGCTTCCTG TTCCCTAACCCAGCAGAGCCCCAGCAACCTAGAGCGCCCTACCTAGCCTCTTAAT

WI-8827	22 C T	TCCTCTGGGAG ACTATGG	GGGATTAGGAT TTTAGTGTTCA C	GGTGCCCTGGGAGACTATGG[C/T]AGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTTAGTTCTCTTATCCACCCAGTCTTCT
WI-8833	51 A T	TCTTCATGCC ATTCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCCTCTAAAGCTCTGTAGACTGTCTCTCCATGCCATTCTCTG[A/T]TGGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAAGTGGCTGTGCATAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTATGCCATGTTGGTAAAGTTCAATTTTCAGTACATGGGTAACACCCAGGCCCTTTCC[C/A/G]T TATATCCAGGTATGCTACAAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAATTCAGTTAGTTGGTTGTCTAATGCTCCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCCTGGCTGTTGGCTCTCGCTGCTGCTGTTTGGTTCTT TCTCTTCTACTGGTCTTTCTTTGCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG AGGATA	AGTCTTCTGA GCCTTCCAT	ACTTTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGTGACTGGGAATCACAGGCACAGACTGAGGAAGACAGTCATGGTGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGAGATCGAGCTTCCATATAAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGTGACTGGGAATCACAGGCACAGACTGAGGAAGACAGTCATGGTGAACAACAACATGCT TCGGACTTACCAAAGGGAGATCGAGCTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAT[A/C]CTCCCGTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAAATTATACAGGGATGCTCAATCGCTCTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGGACTGATATATTGTGAATATAATAAACTCTTTTCC AAGGCTCCCATGGCTGGATGTACA[A/G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTGCTCACTC TCAACTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCAACGGCAGACCACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTCGCTCAGTCACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTATATCTCAAGTAACCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGG AAAATTATATCTCAAGTAACCTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAG[C/A/G]TCCCTCTCTGCCGTTGTACCCACATCCACAGAGCA GCCCTAGTGCAGGTGCAGCCACTGCCACCCACGGCACAGGGAACAGGACCATGCTGC

WI-12108	40	C T A T A	TGAAAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[T]GAAATACTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTTAA
WI-5989	29	G A CACAGGCA	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACCGTCCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCGTGTATACCCCATATATTAC CCCTTCATGCTCCTAAAGAGACATTTCTCTTAGAGATTTTCATTTAGTGATCTTTAAAAAAAAT CTGTGTTAACTTGCTCCATCTTTCTTGGTGAGGACACC
WI-12201	61	C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCCTTTTCTCGGAGTGTATGTCCAAAGCCACTGATCACCTGCATG[C/T]GCCA GGTATGTGGTGGGGTGTGATGGACGTGGTTTGCAGCCCTCCACTGCTCGATAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGAGGAGCCAGCTCTGACTT[A/T]CTCTCTGTTCTGTCTCATCTCTCCCCACATACCA ACTTCTTACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G C C T C	TGGCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTCGTTTGTATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTGCCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGGG
WI-15407	92	A G T T	CATGCCCTTTA AGGATTAAGT	TCTTTTCTCTTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATTT GTTCTGCTCAT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATCTGTATACAACATGGTGTGACATGGCTACACTTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTGCTCATAAATTT[C]CCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTTC AAAAGCAATT	AGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCATTTCAACAAAGTTAGCGTTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T ---	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATAGGAAATTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAAGTGAACACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCAAGGGAGGTGGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTTCTGGTGAATCTTTTAAAGCAGGAGGAAAAATCCAAATAAATTTTTTAA[A/G]AAGGTTTAGCTATTCCCAATGCTATTTAATACAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGTACTGGAGCCCCG
WI-11324	40	C G T G T G C C C C A	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]AGAGCCCCAAAGCTTGTATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTAICTGTCTTGTC

WI-11352a	69	T C G	AGCAGCAGC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGTTCTGTTTCCAGAAGGAGAGAGAGATCATCTACATAAGCAGCAGCAGCATAGTGGAA AGTTCGCTAAGTGTCCTACGAGAGGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCAATTTGCAATCACCTGTGAAACCTATGAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGTTCAGTTCGCTCAGGCGGGCTGGACATCCATGTTGGGAAGAGTTGGCGGGT GATTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAGACTTTTCATATCTTGTTTTTTAAAGTCT TCTTCAGTTCJAGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGATAAGAAATCAGC
WI-11388	88	C A AAGTTC	TGTTTGAAAT ACACGTAAC	TGCCCTGTATC CAAGTTAAAT T	TCATGTGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTTC[A]TATAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T G ATAATAAC	GGTTATGTT CTTGAACCTTA	GTACATTACG TGTTTTGTAAA AAG	TTCTATCATTCCTAAATGAGGCGAGGTTATGTGTTCTTGAACCTTTAATAAATAC[T/G]CTTTTACA AAACACGTGAATGTACTTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACGTGT CATACTCTCTCCCGAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGT	AGCTTATTTTC ATATCACCCA TC	AAAGAATAAGATGGCATTGTTTCAGTTAATTTTGTGTTTTTGAATGGTGT[T]ATGATGGGTGAATA TGAAATAAGCTTACCTCATCCCACTCTAAAGGTAGTTGGTATTTTGAACCGTTGTCAAT
WI-11441	100	C A CAGC	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGCAGTCTTCCCACTAAACCGTGAGTTCAGTATGTCTGGCAGCAGTCTGTCTTGTCTTGGTG TATCCCCATTACTGAATCCCAACCAACAGC[C/A]CAATAAGGCCCTGGCACAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T TTTATTTGCA	TGAGAAGCCA TTTATTTGCA	GTTTATTGTTA TAAAAATGAC CTACAACTT	ACTTTGAGAAGCCATTATTTTGCAG[C/T]CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACCTTCTATTATCTATTATCTCTCACATACATTT CATGATCCCTG
WI-11364	35	A G ...	GGCAGCAGG AGCAGAC	...	TTTTCTTTTGTGCTCTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTGG TCCCCTGTTAGACAACATACCTTCTTTGAAATGTAAAAATGTCA
WI-11276	41	A G AGCAGAC	GGCAGCAGG AGCAGAC	TGCTAGTGGG GCGGTG	AGGCAACACTGCTTTATTAGGCGGGCAGCCAGGAGCAGAC[A/G]CACCGGCTCCTCAGTACACATT OCCCCACCCCTGCTCGGTGCTCCCACTCAGGGCTGGGATGGAGGGGCGAGGTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTGC ATATGTTTTCC	ATTGGAAACAACTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATACTGGGAAAAACA CTATTGCAT[A/G]GGAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTAGTTCAATCATG[A/G]TACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAGACAC	AACATAACCA CCTGTAATTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATAC/C/TGGTACAAAATT ACAGGTGGTTTAGTTTATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTTGGCTATAGGTGAGTGGTTCTAAAACCTTGAGCTTGCAAGAGAACACTTGTGGGGCTT[A] GTTCAAACATGGACTGATAGGTCCACCCAGATTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37 C A	GTGGCAGGAA AAGAGGAA	TTGCAGAGGG TTCAGG	GGAACAGACCTGATCCAGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGGCCACTTTTGAGATTTCAAAA
WI-13416	71 C A	AAATTTTGG AAGTTTTTCAG AAA	AGTGTTTATAG TTCAATGAATA ATTTCAA	GAAAGGCTGTAATTTTATTTCAAATTTTGGAGTTTTTCAGAAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTTCAATTGAACATAAACACTTAGCAGAGGAGGACTTTTIGAT
WI-12310	46 G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTGGGTCT AAA	TTTGAAAAGATGCTGAAATTTATCCCAAGTATAATTTAAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAAATTTCAAGTTTACAAATATTCAGAGAGGCAATTTCTTAAAGCAG T
WI-12086	72 C T	CCGGAAAAC TTGGATTT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACACAAAACGTTTCCGGGAAAACTTG GATTTC/TCCAGACCCGAAGACTCCTCCAAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCC	ATGCTTTCACAGTTGTATTTTGTAAAGAGTTTGTCTATCTAAATTTTCATATTTATGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTGT[G/GGGGATTTGTACAGACTTTTCTC
WI-11585	79 T C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTC	TTAGAGGAAAGAAATAAACACCGGTATGGGAAATCAGTTTCAGAGGTAGGAAAGGAGCTGGGTT TGCAAAAACAAAAIT/CJGGAGATATCAGTGAAGCATGGCCTAGAAAGTCCAGAGCAGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCTGAAACTTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGGACTTTTCCATGAAAAATAATTAAGAGCTAAGGAAATTCGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTCACTGTGAAACTGCAAC[A/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTTG	AGGTGGGAAC ATGCC	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTACTAAGGTCTTCCACTGGAACATGAAGGTAGGGATAAGGTACAGGATAATATACTACAG ATATTTTAAAAATAAAIT/CJTTACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTGCTAC AAGAACAAATTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTACTAAGGCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTCACAGGATAATATACT CAGATAATTTTAAAATAAATTAATTAATAAAGAAAATAGCCATACCACATTGTTCCATTGCTAC AAGAACAATTTGGCAATGA
WI-11627	23	T C	CCTTTCCTCC ATTGCTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCCCTCCATTGCTCTC[T/C]CTTGAGATGGGTTGCAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACATGATGCCCTTTTGTCTGGCTACTTCCATTGCGATGCAAGTCCATCCATG
WI-11636	61	A G TCCT	GGACTTAAAA AGATCTGCTTA	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[G/A]GTA TATCCACATAACTCTAGTTGTTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCCTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTACTCTGACCAT[G/G]ATAATCATCTT TTTGCTGGTCCAGGACG
WI-11654	37	G C CTG	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCTGCAAAAGACTATTAGCAAACTG[C/G]AAACTGCTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTTCATCTACTCTCAGAGTTTACACTCATATTTTCATATTTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A AA	ATTGATTTTAG AAGGAATGC	CAAGGCTTGT CCTCAAGTAA	ACCTGATTGATTTTAGAAGGAACGCAAG[G/A]CTTTACTTGAGGACAAAAGCCTTGCTGCAAGTTGTTT AAATGCTCTGAAACAATCAGATCCCAGCCTGGAT
WI-11680	55	T C ...	TTATCACAGC AGGGGACAG	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCCTCCCTTTT[C/TT]GTCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACCTTTGACATCTTTATCACAGCAGGGGACAGT[C/A]AGGTTGGCTTCTCTA ATGCCACCATCTTGTTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA	AGAACAACTT AAGCAAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTTAAAATCGAATAATACTGAAATAACACACAGC AG[C/T]TTTTCAGTATAATTTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGTCAGA
WI-11706	60	C T	TGGCTGGAATT TTCCTCTCT	ATCACCAAAG AACAAATTCCA	TGCTGATTTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTCTTGTACAATTTATTTGGCTG GAATTTGTTCTTTGGTGATTGTCCTCTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCAAGCTTCCAGGCACACAGCCACCCACACTCTAGACACGCCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCAG[C/A]CTCTCTCCCTCCTCCACACACTCCTTC

WI-11715b	123	C T	AGCTT	AGCTGGCTGC	TCCCATCTG TGCT	AGAATGGAGCTGTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTC/TAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49	A C	AAA	GCACACAATG TAAACACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTGGGAGGGACATGCACACAATGTAAACAGACAAA/CITGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGAAGA
WI-11727	43	G C	TCAACA	AACAATCCTT AAAACAACCTA	OCTGTGGTTG TGTTGCAG	CTGGATTTCCTATACCTAACAAATCCTTAAACAACACTATCAACA[G/C]CTGCAACACAACCCACAGGC AAATGAAACACAGATGCCCCAGACAGACGCCACCATGGCACACAC
WI-11728	16	C G	---	ATCTGTGGTTT ATCGCTG	---	TTTATTTATCAAACT[G/C]CAATTCCATTTACAAAATGTAAATTATCATCAGCTCCCCATCCACTTT CTCCATCTCTTATCTCTTTCCACCCCTACACTTTCTCTCCCTACAAACCCGGTTCCTCAA
WI-11758	61	A G	ATCTGTGGTTT TGCTG	GCCTCACAAA GTATTTCTAA	TGATTGGCCCT GTGGTCTA	TTTTCTCTTTTATTAAGTCGCTATACCTAACTAGAAAGGAGAACTGTGGTTTTCGCTG[G/G]TAG ACCACAGGGCCCAATCACACAGCTCTTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37	A G	AATATA	GTATTTCTAA	AAAAGTGCTCA TCTGTGAACCTC T	CCGGCCTCACAAAATTTTCTAAATATAATTTGCT[G/G]TAGAGTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C	---	GGCTCAGAGA GCAAGGGA	---	AGCATGATATTCGCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAA ATTATTGCCTCTTTTTCCTCCCT[G/C]GTGATTGTTAATAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G	GCAAGGGA	CCCACTTACC AAACCTCTG	AAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTAATTAATGGGCTCAGAGAGCAAGGGA[G/C]G/CACACAAAATTTACAGTCTGA GTTTGCAGCAGAGACCCCTCTCCACCTTTTCATGCCTGTGTGTACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G	AAACCTCTG	GCCTCAGAGA GCAAGGGA	CGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT[G/G]CTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A	AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T	AAGTTAAA	GTITTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTAACTAATTTCCATTTCTCCCTTTTATAGTTTTTAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA[C/T]TGACAGCACAGTTCTTCAAAGTTTGTCTATAGACAATCTGA AAATGGGTTCTGAACT
WI-11906	52	A G	ATCTGAA	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTATAACATCAAAAGAAAGAACTCTGAAT[G/G]TGAGGGAACCTG CAGAAATTAACITTCAGTCTAATTTCTCAGAAATGCCAGAGTAAGATGAACCCCTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTTG GGTGGTCAAG/GTCTATTACAGAAATCTCAGAGGAGGACAAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGCAAGATC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCAATTAGCATCAATTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA/T/G/GTT TTATTAGTATATAAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACTTTGTCTCTGGAGAC/C/CCAGCTAGTCTAAGAAAACTTCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAAATCACAAGTACAACACTGCTTATTTTCTTGTCTGAAGATCAGATCTCTGTTTATTTAA/T/ G/ATCAACATTCACCACAGCTGAAGGAAATTTAACTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAACAAATCATTCTATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA/T/AJAATAAAAACTACTGTAAACATTTCTCTATTTCTTACGA ATACCTTCTTTTGATATTGCAATTTCTATGGCATACACAGAGGCACCTCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAAAAACAAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGGAC/TJAGACTTCAGAGGCATAGCTTCCCTTGTAACGTTTTT AAACATCTTTTCTATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAAAACATGGTAGGGAAAAGTTCTCACTCTGCACATATAAAAAAGGACAGCCAGATATCA AC/C/TJGTTACAGAAATGAAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAG TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGTAT/GJGTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACCTTTTCCCAATTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTTTGGAAATAATGGAAGAGGAGCTAGGACAAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAAGTA C/C/TJGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAAAGGAA
WI-11070a	110 G T	CAGAAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTTTGGAAATAATGGAAGAGGAGCTAGGACAAATTTCTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTT/GJGGTGCAGAGAGGTACTCCAA GTACCCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAAAGGAA
WI-12020	121 T C	---	---	AAATCTTTATATTTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGGGAAACC AGAGCCAGCTATTAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT/T/CJCTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142	GA	---			CATGGTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT G
WI-11076a	106	TC	AGCA	AAGGGGAGC	TCCTGCTCTGG GTATGTGAC	CATGGTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGCATGTCTGTCACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT G
WI-14263	49	TC	GGCATAATCA	CGCAGAAAAA	GGTTATTCAAA AATTAGTATGG GACA	ACCTTTAAAGTTTCTCCCACTCTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCTCATACTAAAT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTCCTCAAGTATAAACTCGTA
WI-14267	28	TC	---		---	GATTTGTTTTATTCAATCTCGCTTTTCAATTTTGCTTTTAAATAGAACATG[A/C]TGTGATTTTAGTA TATGACATCATCATGAATTTTCTCTTACTTTGTTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108	CG	TTCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT TCCTTTGGA	ACCTCTTCTGATGACACTTGTAACCTGTAGGGGCTAGAGAGAAAGAGTAGTAGACTCTACTTTTGC TACAAATCAGGATGCAGGGCATGAGAGGATTCCCTCTCTC[G/G]TCCAAAGGGAAGAGCTTTTGGC AATAAATGGAAGAAAGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTCTTGTTAATCTGGAGCA[G/C]ATTCAAGCAGCAAAATTTACTGAACACTTGCTATGTGCTG G
WI-13951b	88	GC	---		---	AATAAATGGAAGAAAGAGTGAACAAAGTAATGAACAAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTCTTGTTAATCTGGAGCAGATTCAAGCAGCAAAATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	CT	CAAA	GGAGTGAACA AAGTAATGAA	TTCTCTGATC TGGGTCT	GAGACCAAAAAAGGCTCTGCCCATG[A/T]ATTCCTGCTCTCCCTCCTGACTGACCCAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCTTCTCTTGGATCTGTGAATATAACCA ACTGTCTTGTCAATGGC
WI-13264	25	GA	TTGCCAT	AAAAAGGCTC	GGAGGGAGAG ACGGGAATA	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTAACTACTGTTCACGTGCTATTCCTCCTCAAGGAGTTGAGCCCCCTAGATGAC
WI-13960	39	AC	TGATAGA	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C	AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACTTTTGCTCAGGGTCCACCAGGAACAGGCTCTGGCT
WI-15843	62	CT	CAG	ATCTTATAACG AAGAAGCCTT	CTCTGGCTCAG ACTTGCTCT	

WI-13983	52 G A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCAGTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCCTTAAACCTT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGATATGCACTCACTGACTTACAGAAATTAGAACATCCAGGCACTCACTGAGA
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGAATAAATAAGATGGACTTGCAGGTGTAAAAGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCTCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTTCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAGAAAGGCCCGAAATATGAGTGAGACTCA
WI-14284	55 C T ---	---	---	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85 G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAAGAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACTTGGTGGAGGGGATA CCGCTGCTATTCCAGAT[G/C]AAGATTTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33 C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTTGTAGTAGTTACCCCACTAATACAAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG AAAATTACTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42 T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCAAT[C/J]AAGCAAGAGAGTGAAGAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCCAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84 G A ---	---	---	TTATTTGTCAGAAATTTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTGAGGAAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29 T C ---	---	---	TGAAAGGATACAGAAAAAAGTCAAGCAAGT[C/G]GAAAAGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACAGCTTCCAGTTGCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52 G A ---	---	---	TTTTATTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACAGAGCT
WI-13477b	61 A G ---	---	---	TTGGTTTTTAATACCTCTTTGTTGGATAAAAGGACATTGTTTTTTCATTAGCTTGTCTTCAA[A/G]GAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT
WI-13477a	32 A G AAGG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTTGTTGGATAAAAGG[G/G]CATTTGTTTTTTCATTAGCTTGTCTTCAAAGAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT

WI-14297	86 A T G	AATGTTGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTT	CTGACTTTATTTAGCATGCAATGCAATTTATCTGGCAATAAATAATATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[AT]AAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCAATTAGAATCAACA TGTGCACAAAAAGAGTAAAAAT[GT]GACCAAAAAATTAAGATTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGGCGAGTT AGATTCCA	AAGGTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]TGGAAATCAACTGCGCAGAG AAATCAAGACCGATGGTGAATCTGGGCGAGCTTCAAAATTTCTGCCTCCTAAAAACATTTAC CCAATTTTCATTATTGCC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[CA]GTTACATTTTAGGTATCTGGCACAAATTAACCAATGT CTGCCCATTTTGTGTAGCTTTCATACAGTACAGATTTTCATTTGATGTGCTGCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[GT]GTTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTGCAAGAAGAACAGGACTTGATCAAGCTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTAAGGATCAGAGCTTTGTTTACATTTGCTAAAAACCAAGAGAAGAA[AT]JGGAAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCCTTTATTCCAAGAATGGGAAGC[GA]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAAGACT GCTGAATGTCTCTCTC
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	CTCTGTAATGAGACAGAACGCTACAATCTGTCAACACTGGGCTGGACACTGCAGTGAT[TC]JAGGG GCAGGTGGGGCAGGGTGGGCCCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13763	59 T C	GGCTGGACACT GCAATGAT	CCACACCTGC COCT	TTTTTTTTGGTGAGTGTGTTGCTTTCAATAAAGAGCAGAAAGAAACC[TA]JAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTTGATATTTTGTCTTTTCCCGAGGGCAAAAAAGA GAGTCTTCCAGAAACCTC
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAITGGATGGCTGAGGGAG[GA] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTGGTCTCCTCCTCTT GAGGTCCT
WI-13789	62 G A	TGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	GAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAITGGATGGCTGAGGGAG[GA] GAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAITGGATGGTGGTGGTCTCCTCCTCTT GAGGTCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAAA	CCTTTGGGCA GTACTTTT	AATAACAAAGTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATCACAAAAAGC[GA]TGCACAAAAAGTACTGGCGCAAAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40	C T	---	---	GTTTCTCCCACTACTCCGCGAGAAAAGGATATTCAAC[CT]TGTCCTCACTAAATTTTGAATAA CCTAACTCTCCCTTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84	C G A	CCACACTGAA GACTCACCAG	TCCCCACCCCA OCCCT	GTCTCACTTTCTGTCTAGGCTGTAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACAGAA[CTG]AGGGTGGGGTGGGAATACCTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26	G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCCAAGCATCCAT[GT]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGAAACAAGAAATACGGATTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89	G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATAATTA ATATTAAT	GATAGGAAAAGAAAGAAATGAAGTCAATAGTCTTTTAGCAAGCCAACAGTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA[GT]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCOCA
WI-13650	76	A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTITTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTCACAATATTTACAC TTTTAAAC[AT]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAAAGTTACCGG
WI-14319	83	C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[CT]ACATGCAACAATATAGATGTTGGGGTGGGACAGTACAGAATT
WI-13528	80	A G AAAA	CAATACATTT GCATTTTCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAATCAATACATTTGCATTTTCTCTAAAA AAAGAAGACATTT[AG]TTCAGAGAAAACCTGTGGTATCATGCGAGGAAAGCAGAAAAAATTT
WI-13909c	93	A T	---	---	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCAGACT CTCTTCAAACTCGAATATCTTTTTC[AT]GAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G A C	TTCTCAGACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCAGACT CTCTTCAAACT[CTG]AATATCTTTTTCAGAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C A	---	---	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCATCTCTGGACCCTGGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78	T C	ACAGAAAAAT TAAGAAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCATCTCTGGACCCTGGGAACTTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104	G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGAGAACTACCATTATTCAAAATTTATATGT AATACACTCATCCAGATAATGAAACATCTGCGAAAAA[GA]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33	G A T C	AATCAACTAG CTTGCCTTTTG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCCTTTTGTG[C/G/A]TTTGGAAAGACTACCATTTATTTCAAATTTATT ATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAGAGTGTTGGAAATCACTCATCTGTGTC TGTAATCTGCTTACAGTCTTTGCAAGACAGACATATGTTTTTGCATAAAGATATAAATTTGCTTCAT TTTAAACTAAATTTAGTGTTT[C/G]TTTAAATATATGAACCTTTTGGTGAATTTGAACGTGACCAAAAC C
WI-15747	88	T C A G T G T T		TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCCGATGAGTTCCTCTCGTTAAGTGCTGGATATACCTGGCTTGCAC[C/G]TGGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752b	117	C T	---	---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCCGATGAGTTCCTCTCGTTAAGTGCTGGATATACCTGGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752a	106	T C A G T G T G A	CCTTCTGTTA AGTGCTGA	CCCTCCGTAAA AGGTGTC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCCGATGAGTTCCTCTCGTTAAGTGCTGGATATACCTGGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-14339	102	T G T T A C	CCCAATCAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCAACCAATCAACACAGTACATGATTACT[G/C]GGTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A C T G A A	TGGTCTGAAC AAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCCTTTGCCAGCTAGGAGCTTGTGATGGTGTGCTGAACAAAACGAA[C/G]GCTGTGCTTATCTTTC CTGATCT
WI-14061	68	C T	---	---	CCTTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGAGCCCCCGTACATACCTTAT [C/G]AACCATTTCACTCCACCATTTGTAAAATCTCATCTTCTGGGTCTGGATACTCAAAAACAGAT
WI-15719	69	A C C A T T C A G C	ACCTTTTCATC CATTGAGC	TGATACTTGGC AAGAGTTTAA ATT	TTACAGTTGGATTAACTACACTACCACTGAATATACTGAATTAACCTTCAACCCCTTTCATCCATTGAG C[A/C]AATTTAAAACCTTGGCAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTTGGTTCTCTAAATCGATACATCCAAAACCTT[C/G]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T C A C A	ATTTATTAC ATTAACCTTG	GTCTTTTGATA TGTGCTTAGT TTT	GGATTTTATTCACATTAACTTGACA[G/T]TAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAAAGAACATATACAAATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTG[C/G]ATAGTGACACATAGCTGTCAACACAGTG
WI-13785d	72	G A	---	---	TCAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGAG[C/G]CAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG
WI-13785c	56	A C	---	---	

WI-13785b	40	C	---	---	TGTTGTGACAG	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACAGTG
WI-13785a	27	T	C	TGCTT	CTATGTGTAC T	TCAAACTGCACACTATAAAAGTCTTT[C/G]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACAGTG
WI-13793	88	C	G	ATAGG	GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAATAAAAAATAGTTTTTACCCCATTTGATACAAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATATAAATCTATGACTTG
WI-13794	52	A	G	TTCTTTCTC	AGAATGGGCTC TTAACCTTGTA	TAGTCTCTACAAATCCTTCAATCCATTTCTCTCACCCCTTTCTTTCTC[C/G]TACAAGGTTAAGA GCCCATCTTCAACAAACAAAAACAACATAGAGCAAT
WI-15729	35	A	G	GTGAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[A/G]GGCACTTTAGAAAGAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAAGGAAGGTAAGTCCCTGTTTCAGCCCGGCGCTGCTCATTGTTA
WI-13424	66	G	A	C	TTTTTCTCCCC AGGGTCTA	GTCTTTGCACAAAGTCTCCCAACTGGTTGGAGTTTCCCTTCTGAGGTTTTTTCACCCCTATTCTTC[G/A] TACACCTGGGGAGAAAAACACATGTGTAGTGGCTCAGGACATGAGGCAGCCGTTTCAACAAGAT GCTGGCTAAGGGCTTC
WI-14085	29	T	C	AATT	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGAGAGGCAATTT[C/G]AGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGACAAATTTCTGTCTGCTTTTATCTCTGAACATTCCTTGAAGCAGCAA
WI-13446	22	G	C	TCACATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACATCATCA[G/C]CCTTCTGATTTTGATTCCCTTTCTGCTCTGTAATTTTCTTC TTCCCTTTTAGGGCTAGTCTGTTTAGAAATTCGTGTTTTGAGAGTAGTGAAGCCCTTTTACTTTTTT CTGACTGCCTAATT
WI-13725	56	A	C	TGGGTGOC	CCTGCTGCTC GGGC	TCACACAAAGGCATTTGGAATGTCACCTTACACATGGTGAGCACAATGGGTGCC[C/G]GCCCGAG ACAGCAGGATAAGTTTCAACAACTTGACAGGCAAGTTAGAGCAAGGCATGGTTTCAGGATG
WI-15702d	107	T	C	---	---	CAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[T/C]GGGTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T	C	---	---	CAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[T/C]GGGTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C	T	---	---	CAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[T/C]GGGTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C	AACAAAATAA AGGCTTTTCAA	CCTCACCCCTT TACCCC	CAAATGTTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTCAAAGAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAGAAACTGTAAACCCTGTAAACAATACTAATGGGTCTTTGAACAAAATAGTTT TGA
WI-13831b	113 T C	---	---	TTTTTTTTATGGATGCACTGTTACATGTTTTATTAGCGAAGGTGACTTGGAAAAGGAGATTACACAT ACTTCCACTGTATCCTCCGGTAAAGTTTTCCCTTCTCTCTGTAGAT[C/G]TCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13831a	56 G C	---	---	TTTTTTTTATGGATGCACTGTTACATGTTTTATTAGCGAAGGTGACTTGGAAAAG[G/C]GAGATTCA CATACTCCACTGTATCCTCCGGTAAAGTTTTCTCTCTCTGTAGATGTCCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13806	62 G A	---	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACACTAGGCCTCAGGT[G/A/C] CCATTAAAGCATGCTGTGAATGCAAGGAAAAGCTTAAAAAATTTTTTAAAGGGTGACTCCAGTAAA CAT
WI-14372	86 A G	---	---	CACATTTTCAGCAACAAATCGAGGTGCAACACAGGGTTATTTCACATTAATATATTAACTGGATTT TTTGTCAAATAAATAGGGA[A/G]TTCTCTTTAAATAACCATCTCCTCACTTCATGGCCAGT
WI-14373	95 A G	---	---	AGGCTGTTTTTGAGGCCTGAGGCCCAACATGACAACGTAAAGACTGTAAACCATGGTGCATGTGAGTT ATGAGCTAGGAACCCCTGGACGAAACCA[A/G]CACATATACAATCATCTCCACCTCCCAACGCCTTT ACTTTCACAGCCTCTGCA
WI-14078	61 C T	AAAGAAGTAA ATTAGGAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCCACATGGTGTATCAAAGAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGCATGGAGGAAGGACTTTAGATGGTCACG
WI-14083	47 C T	AGACTTGAGA GCTTAAAAACA	GCCTACTGGAC CTCTAAACTAC	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACAACACACT[C/T]ATTTGTTATTTCACAG CTCAGTAGTTTAGAGTCCAGTAGGCTGGCTGAGTTGTTGCTTAAGGCTCTACAAGGCCAA
WI-14085	31 A G	CATTATTTTC ATGTGTAAGA	CAGTCATGTC ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAGAAGAAAAC[A/G]TAACCTAGCACGTGAACATGACTGCGATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAAGTGAGTGAAAACAAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCCTT
WI-12169	121 G C	AATAAAACTT CCTATTTTCTT	GGGTCTGAGG TGAAAGAAAA	GTCAAAGGTTGGCAAATTTTATTTCCACTTATCAAGAACTTACAAAATATTTTTGTTTCATTTCTAAA TTTTCCACTTATTGCTAAGTTATAAAAATAAACTTCCTATTTCTTTTGCTT[G/C]TTTTTTTCTTCA CCTCAGAACCCCTTA
WI-15705	50 A G	GGAGGGAGAT TTTAGACTGA	AGCTGTAGTCG TCAAATACTCT	TTGTTTTTATTTGGGGAGAAATGAAGGAGGGGAGATTTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCTCTCTCTTTGTACTACGGAGACCCTGCTTATAGCCCCAACACAGGAAATCCTCA TCTGGGTTGCCAGACAG

61-

WI-14379	102	C T	TCTATTAACA GGGTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA	TTTATGCTGTTGTTTCTACTGGTGGTGGTCTGGCTCACTAATATCCAATCCTAGTATGATTTTCTTT TACTTGTGCTATTAAACAGGGTTATGTCACACC[C]/TGTCAACCTCAAAACAGATGATACT TAAATAAAACAAGCAGAAA[C]/A]CCACCAATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	---	---	ACCGCAGAGCTGCTGTTTAAAA[A]/G]ACAAGCGTCTGGATCTCTGCAGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCAGCTGCTCTCTCCAGGACTCTTCCACCAACCCC
WI-15937	24	A G A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	TGAAACTGAAACGTTATTCCTCCA[A]/C]ACACCGTAGAAAATTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGGCAAAAAGGAAGTTTCAGGTGATACAAGATGCTCCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	AAACTGAAAC GTATTTCTCTCC	GGCCTTTAAGT TTCTACGGTG	ATGTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A]/G]TATTATTCAAATGTGTTTCAAATACTCAGCCAGAT CAACAAAGCTCAGTCACTAG
WI-14124	92	A G	---	---	GACAAAGAGGCGAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTATCAGAACGGGTTGGTTGACCT GCATAGATTTTGTGACGACTA[C]/TGTGGCCATGCCATTCTGTAAAGTGAATTAATGAACA GTTTATTTCTCACAGTTCTGGAGTTAGAAGCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGCTTCCATG[A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14138	23	C T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	TTGTTGTTGGCACCAAGAAAGCT[C]/TATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTCAATG
WI-13551	74	G A	TCCTTCAGTAG TAGTATTTCA GACAATC	GCTCATTTCTT TTAGTGCTAAG TAATATT	GGCAGGTTTATTCATAATTTTCAAAACTTGGAAAGCAACCAAGATGTCTTCAGTAGTATATTCA GACAATC[G]/A]AATATTACTTAGCAGTAAAGAAATGAGCTATCAAGTCAATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59	C T	---	---	TTTTTAAAGAGTGCTTCACATCATTTATATTGTTATTCACACAAACTTTTTTAACTC[C]/TGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953a	26	T G A T	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTTG A	TTTTTAAAGAGTGCTTCACATCAT[T]/G]TATATTGTTATTCACACAAACTTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC

WI-14631	82	G A ---	---		TGAATTC AATGGACAGTTTGGCCTCTGTTT TAGTGAACCCCTCACAAGCACTCTGCATAGTCGCTTT CTGCTCTCTTTAACTGATGCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCTCCTCAGGGCCTT GTCTGA
WI-6053	24	A G ---	---		ATCACCAACCGTGTCTAAGAACAAAC/GTCTTCATGTCTCAACTCATATCCCCGGGACCTTTGTCAACTG CAGTACACTTCTGCTGCACTGACCTGGCTTCTCTGGAGGAAGCCTCTAGAGCCAGGTAAGGGGGTGC AGCAGTAGGGGTATATCTGGCTGGCAGTTGGAACCCAGGAG
WI-15964	99	T A CTGAGGTA	GACTTCTCCAC CCTCTTGC		CAGAAACCTCTTCTGTGTTAATTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGAGGAGGCTGCCTT GGAGGTAGTAGCTCTCTGTCCCTGGAGGTA/T/A/GCAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103	G A GGCAC	CCCTTCTTTC TCTTCTTC		CAGCTAAGGATCACTGCAGCTAAATACAGATAGAGAAAGCAAAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGCCACGGGGAGGCG/G/A/GAAGGAAGAGAAAGAGGGGAGGAG OCT
WI-12179	96	G A TGGAGGTCA	TGGAATGACCC TGATAGTC		TAATTTAAACACGCCCTTCCACATAGTGGTGAGGCATCTGCACATTTTCTAGAAAGGACATGA ATAGTGATGGAGGTACGGTGGAGGTCA/G/A/GCATCTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	GGAGATATTGA TCTTTTCTGA CTTATT		CACAAATAGTGAAATTAATCTGAGCAAGAAATCATTTCTCAATTTAAATTTGTTC/GIAAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACTGTTA
WI-14666	105	T A ---	---		AATGTGGACTTTCACAAAGGGTTTAAACTAATCTAATACTAATCTACAAACACATCCAGAGCAT TATAACAAGAAATTTTACAGGCAGCTAATGTATTAAAT/A/AACCATGAAAAGAAAAAATCTG ATCTAGATGTCAGCAATGGGTGAGACTGTCTTGTCTGGTAGATGCAGTGTGTGTATGTTCTAC
WI-13473	31	CT ---	---		TCTATTACAAAATTAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATACACAGTC
WI-13967	103	A C AAATAAAAA	AAAAGACTAC AGATACAAGG TG	TTGTGTTTCA TCTCCTAAAAG	AATTTAATAGCAGCTGTGTGTGATTTTAAAGAACAGATAAAATATGTCATTCAGCAGTCATTT AAAAAATAAAGACTACAGATACAAGGAAATAAAAA/A/C/CACCTTTTAGGAGATGAAAACACAAA
WI-14408	60	T A G	GCAGACAC TATTACAGGCT	TTAATTGTGA AACTCATTTG TTACTTT	TTAATATTTACGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGT/A/JAA GTAAACAATGAGTTTACACAATTAATAATTAACACATACTTATGGGATTTGTGAATGA
WI-13683	47	C G ---	---		TTTTGTGTTAAGAACAGCATTTTGAATAATAAACCTATCTGCCCATG/C/GJTTTACAGCCCTTTTAAAT TTGTAATTTTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	CT CGTCT	CATTGAGATAA AGCACACTTAT CAC		TTAGAAAAGTATAAAGCAACACAACTTTTGGGAAAGCACCATTGGCAGTCCTTTGTGCTA/C/T GTGATAAGTGCTTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---	---		ACATGGCAGATACAGAGTGTCTG/A/TCTTGAAGACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGAGCGTTGAAGGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59	T C	GATAACATAA AATGATCATG AGAATTTT	GCCATCTCTC TTTGACTTTT	CCAAACATTTAAACCTATGACTGGTCAATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101	A G A	CCCACITGAAC TCAAGTCATC	AAACTAAAC CTTTGTCCTA AAA	GTGGAATTTTATTAAGCCATCAAAATTTCTTCACACTCAATACTGTGTAACAACAAGATAACACAT CTTCTGCTCATCCCACTTGAACCTCAAGTCATCA[A/G]TTTAGGCACAAAGGTTTAGTTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73	T C	GCGTTTGACTT GTGGG	TCCCACACTGC OCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTTGTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCGAGTGTGGACGGGAGGATTGCAACACAGATTTCATACTG CAA
WI-12535	50	A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTCAGGTGGTGAAGGGTTGAGGTGTAGATAT[A/T]CTTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATGCCGTTCTTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G A	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATTATGCTTGGCTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCAGAAACCATGAGATTTGGTCAAGAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T C	---	---	ACACAATAAATCCATT[T/C]CGAGTGATTAAACCTATTGTTGTTTAGAACCAACAAACACTAC AAGAAACATTTTCAAACCTTTTTTTCAGGCTGA
WI-14808	52	T A	ACCCACCACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACCTTTAAGCAAACAGTTAAAAAGTACCCACCACACTACCTGT[T/A]AAAACTTAAC ATTGTGATGCCCTCTGCATCAATTTTAGAAAAACAAGAAACACACAACTGAAGGCCCATGTA
WI-14816	29	A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTATTT[A/T]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-12542c	71	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T	GCTATTAGGC AACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATG[T/C]ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTCTAGAAACTGGGGATACAGCAGTAAGAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATTTCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TC TTG GAG GATAGAGACAGAGTGTTC/C/GTTGATTTTTCGTTTCGGTTTCAGTTGGTTGTCATT GGTTTGTGTTTGTCTAATTTTGGCCACCCCTATAAAAGCAGTGCACCCAGAGGCAG
		TGGTGACACG GAAATACTT	TTTGTTGCTA CTTTTACAAA CTTT	ACATTCCCTTATGATAGCAACAATAATATGATGGATGGTGACACGGAAATACTTAATATTTAA AGTTGTAAAAAGTAGCAACAAAATTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14856	60 A T A A			ATGGCAATTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTCTG/GA/G TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
WI-14863	61 G A ---		---	TTTTAATTAAACGTAAAAAGGACGACATTTCCAAGGCTCTCTAACAT/C/GAGTGTCTGACGCCCCA TTGCTTTGAGATGGAATGTGTTAACCCAGGGTGA
WI-14867	46 T C A	GACATCCAA GGCTCTTAAC	TGGGGCTGAG ACACTC	ACGGAGTGGTCTCTGATGTATCTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAATT AGAAAAAATCCAAATTGACAGATATTCTGCA/GA/AAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTCAG GCCATTIAT	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTATAAGGTGCCACTAAGGAAA ACTTCTCCAT/C/AAAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCTGTCTCTGCT
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/C/AGGTGCCACTAAGG AAACCTTTCTCCATAAAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGCTT
WI-14898a	50 A C CA	CATGTACAGG AAGAGTTGTCT	AAGTTTCCCT AGTGGCACT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/GA/ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCCATCAATCAGTGACTCCTGCACTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTTCAGTTCTGTTG/GA/AAAGTCTTTTC CTGGTTGCAGACAGATACCTTGTCTGTATCCTCACAATGGCAGAGAAAGAGAGAAATATCT
WI-14911	52 G A C	CCAATACATT CAGTTCTGGT	CAAACCAGGA AAGGACCTT	CTGATGCTTTGACATCTGGGCTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCCAGCCAAATTC TAGTGATAGTAGAGGACTCA/C/CTGCACTGACCTTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAACCACT
WI-14913	88 C A ---		---	
		CTGGACACAG TTTTCTTAGC	CAAGCCAGGA CAATAAATTC	ATTTCTTGTATGGCTGTGTAAGCCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA/G C/GAATTTATTGCTCGGCTTGATGGCTTTCACAGC
WI-14914	66 G C A			GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACTTAGCGAA/T/C/ACTTGTGGACCCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTTCAAAATAAAATTTCTTAATCAGGTCCA
WI-14926	49 T C ---		---	

WI-16083	89	C T	ATGTTTAAACA CAACATATC AAGGAT	TGAAAAAGATT OCAGCC	GCATCTTTATACCACAGAACTCATTTATGTCTTAATCATGTTTAAATATAATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATCTATAGAAAAGCACTAACCATC CATTAAGCAG
WI-14930	55	C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAAAGCTCTCTCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGTTGTGGTGATTGGGAGCACGAGGAGAGCAA
WI-14946	47	T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTGGCCCCAGACATAACAT[C/T]CTCTAAATCATCTCTA GATCAGGGAGTCATAAGGACCATTAAAGGCTCATTAAGGCTATTACACACAGTACTTTATGGAAGGATT
WI-15987b	80	A G	---	---	ACATTAAACACGACACAATTAAAGGGTCCCAACGAGGTTGGTAGTGCCCTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]CTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C T	CACAAATTAA GGGTCCCA	GGAAGGCACTA CCAACCTC	ACATTAAACACGACACAATTAAAGGGGTCCCAACGAGGTTGGTAGTGCCCTCCACTATGTGAGGAC CACTAAGAAAGATGGT[C/A/G]CTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T C	AGGAAACTG CTAACTTGTC G	GATGATCTTAC ATCAGTTGTG GA	GAATAAAGTTCTTATGGCGTTCTCTCAGGGAACAGGGAAACTGCTAACTTGTCTAGT[C/T]CCAAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAGGCTTGTCTCCCTCCAGCTGA
WI-16100	52	A G	CAAAAAGCTA TTTCTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTCTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTCTGAAATC
WI-14958	83	A G	AATAATTAT CTCTTCTTTT CAAGG	AATGCAATCAT TTGGGTTTT	GTGATTGATCTGTAATTATTGGGATTATTTCAACTCTAAAAATCCCAAGATGAAAAATATTTATCT CTTCTTTTCAAGGG[A/G]AAAAAACCCCAATGAATGCATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAAATTCAGGA
WI-14976	35	C T	GTTGATTGCT TCGTTCAAAG	TCAAACTAAAT CTTCCATTCTA AGC	TATTTTAAATTGGTTGATTGCTTCTGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAAGTGGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31	G T	TCAGTGGTGT TATTGGATTTT	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGAATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTAAATCATGCCTACCAGCCCCATCTAAGCCAAAATTCAAACACCCTCTGCTGCTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAACGTA
WI-15002	72	T A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAAATGCCTTCTTGA TTTCCT[A/T]TCAGTTTAGGCTCAAAATGGGCTCTCTCCTCAAGGCTGACCTCAAAGGCCAGTT
WI-15000	90	G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACCT CATGTACCTAT TTCCTACCTG	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGTTAAATCTTATCTCTTTTTTATACACAATACCTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCCAGTGCAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCCACGCCATCTAAAGCTACTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA/AJTCAAAAAACAACACTGGGACATGCCCTGAAATTGCAAGT TGGAGTTCGTAAAGATCTAC
WI-13470	100	C A T	CCTGCCTTAT ATTGGAATTC A T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCCATGCAGT CAAAATTCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACCTCAGCCCTTC
WI-14712	38	T A CA	TGAATGCTTC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA/T/AJCTCAAAATACCATATACACATACT TTCAATCACAACCTCAAAATATAAAATAACCTACAAATCACAATTGC
WI-13712	40	A C TCTATG	TTTACTTTGTT GTCATTTTAT TAT	CCATAAGTCT CACACTTTCT TAT	TGGGATACCCCTTTACTTTGTTGTCAATTTTATTTCTATTG/AJCTTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATGGGCAATATGCAATATAATATTGTGTTGTTAAAAATTTATGCAAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA A A	GCTGCCAATTA CAITTAACCTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA/C/AJATTGTAAGTTAATGTAATTTGGCAGCAT GCCCAAAGTTTAAGAGGACTATTTCTTTAAACAAAGACAGTGTCTGACATTTATTTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTTGCAATTTGAGTGTCTTATTATATTGGGAATTTGCAGTGATTTAACATTTGTACAAAT GCACAAAATCTTGCTCTCTTC/T/AJTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTTGTCCAT
WI-16167	58	T C GATTTT	CGCACTCTAA ATTAGAGATA T	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTTCTGATATACATTT/C/CATCTT ATTCACCACGAGCACACACCGCACAGTAGAACAGTTCCACACCTGATAAAATGACACAAGATG
WI-14482	17	G A	GCAGAACCAATTAATAA/G/AJATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C	TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTTCCAGTATCATGTAC GCACATAAAAAAA/T/CJGTGTGCTTGTCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C	TGAAGATTAA CCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGGC/AJCTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T ATGT	GCAGCAAGAT TACATCAGTA T	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTT/G/TJACCT TACTATACTCTAGGCTATTTGGAGTGTTCCTCCAC

WI-15100	74 G A ...			---	TCATTCTAGTGGACTTTAT	TCTTATTCACAGCCAAAGAAAAATACCCAAATTTTCCAAATAAGCAAAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCOCTCAAGACAAAGATGGACAGCGAGCTGGTTCTGGGGT
WI-14492	92 A T AATTACT			GTCAACATGTT ATATTTCTTT TAAGAC		TGGTACAGAATGTTTAATTACAGCGGGCAGTGATTCAGTTAAATAAAATTAATAAACCTTTATTTT CCCAATATATAAATTAATAATTA[A/T]GTCTTAAAGAAAAATATAACATGGTGACAGCTTT
WI-12002c	89 T C ...			---		TCATTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-12002b	68 G A ...			---		TCATTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-12002a	30 C G GGACACAA			TGGTTTTGGG TGTTTTCTT		TCATTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-15116	96 C T GTTGCAGTAA			CCTGAATATGC AATTATTTATT ATGACA		TTTTCATTTATTTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTACATATAGAATTAACACTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAATAATTGCATATTCAGGATTTTG TGAAATAGGTGATTTGGGA
WI-12578	37 C T AATGGGAA			TCAAGCGACCA CCAACAC		GCAAAAGCAAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTGGTGGTCGCTTGATACCTGGT GCTTGTGTGATGGAGCAGAGAGTCTCTGCTGTCATGCAGGGCGTCACATATTTTAACGTGCACTAAT TTGGGCAAACTGTCATTC
WI-15153	40 A G GCATTGCA			AACCTCAGATA AGTGCAGTGT T		ATTCACGTTGGCCAAAGATCTCCCTTATGTGGCATTC[G/A]GAGACACTGCACCTTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTAACCATTTCTCTAA
WI-15215	84 G C TCAAATGGG			CCAACAGGGGA AAAAGTCA		CCTTTGCTCTCTGAACCTGGACCGAGGATGGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTCCCTGTGGTGGAAAACTCTGTGAGGGTTGGCA
WI-15225	80 C T C			TTTGATTGGCA TAATCACTCC		AGGAAAGAGTGGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTATGTGTACAGCACTTGAGGAC CTAGAAAGCAAA[C/T]GGAGTGATTATGCCAATCAAAATGCAAGGTTGGAGATATGCTAAAA
WI-15152	51 G A ...			---		AATTTGCTAGTGCAAATGGACCCAGAATTGGAAGGGCTATGTAACCTACACA[G/A]TATGCACACCAC AGCCATGTGATGTCACAGATCCTCTTGTGCATTCAGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55 C T TAGGATG			TGTTAGTGACA GACAGATAAA CAACAGAC		TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGAT[G/C]GTCTGTTT GCCCTTAAGCAATTTACAACACTCACTGGGGAAGAAACAGACATGCAAAACACGAGATAAAACACAAT

WI-15182	49	C A	GCACAAACAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCACAAACAGGGGCAAAATA[C/A]TGTGGATTAAACCC ATGCTAATGGGTACCTTTATTAGTAATCATGGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGCGCTTGGC ACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATG[C]CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CATTATTGAG TATCTTGGCTT TGAT	GTTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTTATTGAGTATTCTTGCTTTGATT[C]GTCTACGTAAAGCATGTAAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGGAAGTCTGGTATTATGGAATAAACATTTTGTGCTTCCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATAATATGCCCTACATATTTAGTGAAGTACACCCAGATATTTTGGGAGAAGAG TTGTTTGCCTTTTGGCAAAATATGCATAACAAAT[AT]TGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CATTGCAAT AAACACCATC CA	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTGCAATAAACACCATCATTT[C]CCTGAG TCCACAGATAAGGTCCCGGAGAAGGGGCTTCCCTCTCTCGCTGGGTGACGTTCCACGCGGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATT[AT]GCTATTAGCTA TGTTTACAATTTGTCCTGAAGGGGTCTAGATGTGTACACCCAGAAAGTGGTATTCTCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA AA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTT[C]TTGTTTAAATCTCTGGCTTTCTGGCTGG TGAGGAGGCACAGGCTGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCCTCCACTCCCCAG CCACATCTCTGGCTCT
WI-12159	28	C T	AAGACACCGT GCAAAATGC	CCCTCTCCTCA GTGCACCTT	CTGTCCGGGGAAGACACCGTGCAAATGC[C]TAAAGTGCACTGAGGAGAGGGGCTGTGACTC CCAAACCCCTCGAATAATTTATGAATCTAAGAGTCCAGACGAGTTTATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAATGCCTAGTGGCATTAAAGGATGC[A/G]GTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTCCATGTTAGGTGCTTTACTTGGATTATCTCACITTAACCAACACACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/ T]CCATTTAGGCTTTGTTGTTCCATTTAGAGAGCAGGAGAGGAAATTTAGCATAATTTCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG GA	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTGTAAGTGAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGAAATGAGCTGGAGAAATTA TCTG
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCCTCCACCAT GATTGTGA	AAGGTTTAAATGGACTACAGTCCATGTGGCTGGGAGGCTT[C]TCAACATCATGTTGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123	C T	AGTTGGCATTG AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTGAGTATTTCATCCATGGGCTTCTACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCATCAATAGCCTAT[C]TAACTCCATGT GGGAGTTTTCATAATAA

WI-14528	62	T G	TTTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTATAATTTTAACTTTTCTGGATGGTATAAATTTGJTT GAATATAAATTTTAAATTTTATAAAGTCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCCA AGTCTTTG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTCJCAAAGACTTGGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C A	CCAATTTCTAG TGATAGTAGA GGAATCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACACAGC CAATTTCTAGTAGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37	G A	TTTATTGGCTGTCTCTGTAATAACAATGTGGTGAAC[C/G/A]TCTTAAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGTACTGCAAGACCAAGTGTCAAGGCACATAGGCTGATTATCAGTGG
WI-14580	100	G A	CATCCCATCT GTCTTGCA	CCGACCAAGAT CCCTOC	AGAAATTTTTCCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTTCAGAACTTCTCAAATAC CTAGTTATTATACACATTCCTCATCTGTCTTGCA[G/A]GGAGGGATCTTGGTGGCTTAAACA
WI-8540	73	T C	GGCTGCATT TGCTTA	GCCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCAACAGAAAAAACACACAGTACACACAGGCCTGCATT TGGCTTAT[C/G]TGCTGCTGAAAAAGAGGGCCGACCTCTTGTAAAGAATGCT
WI-8039b	97	T C	AAGTAGAACACAATAAGATGGCTCAAAAATATCAGAAATGCACACTCGCACATCAGAGTAAATACTG TTTGGTAAAACCTTGTTCAGTTAAATATGTAT[C/G]TGTCGGTGCATGATGATTAAATATCTTCT TACCAGATCACCTTAAAGAACCAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCCGAGCCGACACCCACA
WI-8039a	87	T C	AAGTAGAACACAATAAGATGGCTCAAAAATATCAGAAATGCACACTCGCACATCAGAGTAAATACTG TTTGGTAAAACCTTGTTCAGTTT[C/A]AAATATGTATGTGTCGGTGCATGATGATTAAATATCTTCT TACCAGATCACCTTAAAGAACCAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCCGAGCCGACACCCACA
WI-8044	107	C A	CACAACATTCAGAAAGTTTCTGCAATGTGCTTCTCTGATGCTGCTAAAAGATTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTCAAGGTTTCTCC[C/A]AGTATGGATTCTCTGATGATTAAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAAGATGGAATCGGCTGAATGCTTCCACACT
WI-8550	32	G A	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAAACTCAAGCCACAACCTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAAGAGCAACTGATGCCCTCAGTGAA
WI-8057	87	T A	TATTAGATAAAACCCCTTGTCCCGATTCCAGGATGTTTAAATTTGCTTCTCTTAAACTCTGTGACTTTT CCTGGTTCAAAGGACAGTT[A/G]ATGGACAGCAGCAGAGGAGTGGGGCTGAAAAATGTAATCTTT GTGTCAAGGCACTCTGTGGCTCACAACCTGCCCTGTGAGAGGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG

WI-6192	91 A	GAT	GACTGCTAAG GATTTAATTG	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATAATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTTGGAT/GIATTTTAACTATTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105 T	A GAA	CACATGGCAA TGATAATAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGTGTGTCTCACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACTT GTCACCAAGAAGTACATGGCAATGATAATAAAGAAAT/GATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAACAAATGGAATTTGAAAAAATAGGAGTAA
WI-6213	164 C T	---	---	---	CATATGCTGCTTATTCTGTAAAGTACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCCACAGAAATGTAGTATGTTGCTTACATGTTT ACTTTGATAATTGCTCATTAATACTATGT/C/TATATAATATGTAATAACAGTAAGTAGGTGATCC TGCATTTGAGTAAAGCGGTAGGTGGAAATCCAGATTTCTCTTTGAGGAAAA
WI-6217	131 C T	---	---	---	CGGGTTAAGAAATACCTTTAAATTTAGGTAAATAAAGCTCAAGGAGGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTCAGTGTGCTCCAGGGCCTTGACAAAGCCTCATTTCAAG/C/T GGCCACCATGGCCCTAGGGTCTGCAACAAGTCCAGCAGCAATCATGGCGTTCTCGTATATCTGATCC AC
WI-6238	175 G A	---	---	---	ATAGTCTTTATTGTCAACGAAGGCTACACGGGATCCTCTGGTTTGTGTTTATGCTTTTTTTTTC TAGAAGGTATCTACATCTGCAATTTATTTACAGCCTTGTGGTATTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAATCTCTCAAAATTTG/AGTTCAGACTTCAGGAAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTGGTGCATCCAGAACGACGTTG
WI-6272	86 C T	TAA	GCATTTATTCA GGGAAACTT	CTGTTTTTGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGGTCATAGGGGATTAGTCACTGTACAGTCAATAATGCAATTA TTACAGGGAAAACTTTAAT/C/TTTCTTTGTCTCTCCAAAACAGCTGCTGGAACACCTCAAATTA GGGATGTTTCATCTAAACACCTTTACTGAACTTGATTCTTTGGCCAGAGGAGGCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTGCGGCAATAAATGAATACTTTGATGCTTATACAGGCAAGAA TCCAGCATCCAGAGAAGCTCTGTCTG/C/AGTGCAGGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTGCGCTCTCGATTCCCTGCCAGCAGTCTCTCTCTCTCTCTCTCTCTCTGCCC TCTG
WI-6303	96 G A	CTCTGTCTGC	CCCAGAGAAG	CAGCCATGGCT TTGCAG	ATGCTTTTGCATGATTTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCCAGCGTGTGATGCTATGCTGCTGCAATCAATCACTGTAATGTCCATTGCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGT/C/TCTGGTT CTTCCCTTTACATTTCTTTGGGGGA
WI-6315b	193 C T	---	---	---	ATGCTTTTGCATGATTTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCCAGCGTGTGATGCTATGCTGCTGCAATCAATCACTGTAATGTCCATTGCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGT/C/AGTGTGCTGCTGGTT CTTCCCTTTACATTTCTTTGGGGGA
WI-6315	187 T C	---	---	---	ATGCTTTTGCATGATTTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCCCAGCGTGTGATGCTATGCTGCTGCAATCAATCACTGTAATGTCCATTGCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGT/C/AGTGTGCTGCTGGTT CTTCCCTTTACATTTCTTTGGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGGAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAGI/GI/TATCTTTTACAAAAAAGGTTAGAATAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAAI/A/GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAATTCAAACATACAAATCAAT TACAACI/A/TATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCTCTGGGCACATGGATCCCAAGAGAGATTTTCAGCAGATTTTCATTATAGTTACTTAA CAGCTAAATAATAAGGGTGTATTTAACTTACTTACAGAGTCACATAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG/GI/TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGACCTTCACAAACACGAAACAGCTAAAACTCTGAGAGAAAACI/GI/CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTACATGGGCTATTATTATTAAGGACATTGTGTAATGTTCCACTTTGTTTTAAA I/CT/AAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCGC
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTACATGGGCTATTATTATTAAGGACATTI/GI/CTGTAATGTTTCCACTTTGTTTT AAACAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCGC
WI-6558a	42 G C ---		---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCTATAI/T/CJAGCAATGGATGCTGTGTGAGAACATAGTCCCAATAAATTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75 T C GTCATA	TCCTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAAACTCCAGCTGTTCTCTGTCTTT TTACTTAGCAAGGAAACCTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA T/CJACCAAACTGAAGGTGATTGAACCCAAATAATGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTAICTGTTATATTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACCAATTATTAAAGGAGAGTACTAGGAAAAACTACCAACACAGCATGTGAAACAGT TGGGCAGGTGGTAAAGGACAGACTCTGGAGCCACAGC/I/GGCTAATACACTGCAATATTTTA TGTTAGCAAAATTATAGCTGGTCTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	TGCGAGTGTAT TAGCC	

WI-6690a	28 T C	AAACCCACC ATTATTAAAGG AGAG	GCCTGTTTGG TAGTTTTCT	TGCTAAACACCACCATTAATTAAAGGAGAGTC/ACTAGGAAAACTACCAAAACACAGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGCGACAGACTCTGGAGCCACAGCCGGCTAAATACACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTCTGTGTATAACCCAGAAAGCGGTATCTGG
WI-6770	53 A G	CAACCCCAA AACATCACA	GCCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA/AGJAATTATTTCAT ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCAATCTCCA AAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGAGGCAAGGTTGAGCAAAATCAGCTAGCACTAATCTTGACCAAAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTTAGATGAATTCACATTTAAACATGGTAACCTCCAAAGCATCTT TCCAAAACAAAGAAAT/AGJAACATTGGAATAGTCACITACAAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG/CAJCTTCTCCTCCAGCTTTTGTGAACAAAAC AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTTCAAGGTACAAGGTCTC
WI-6844	225 T C	---	---	TAAATACTGCCAACTAGCATTACGTCCTCTTGCACTATTAAACAAAGGGTATTTCTCCTTG GTATTTCAAATGATGCATTACAAATAACGAAGTTAGAACTTAAATGCACCCTGATTAATATG TAACTGGTAAATTTGTTTTAAAGCATAATAATTTGGTTCTTCTCATAAAATGGAATTTAAA TATTTCTCTGATAGTCTTGAGGT/CAJATCATATGAGTAGTCAAGGTG
WI-6824	112 A G	---	---	CGGTTTTGCTACACTTAATGGTTTTTTTTAAAGGATTTTTTTCAGGTCTGTGAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGTACAGAGTCTGCCAA/AGJACCTTAGAAAAATTACAT GACACGGAGAAAATGCGCTCTTGCTCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAACCTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C	GAAAAATGAG ATGCAGTTAA AATTC	TCACITTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCAAACATGGAAGTGTCAAGAAAAACATCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAGGAGTTACATATTAGTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC/CAJAGATAATTAAAGCCACAAAAGTGAAGTGAAGTGTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C	---	---	TCCCAGCTCATATTATTTGGGCACAGAGTGGGCACTCAAATATCTGATGAACITTGATGAACGTAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCAGAAAACTTTGCCCTCCCAAGGAATGTGTTCTAATTTGGTTTCAAGCACACACTGGTTCC CACTTTTACCACIT/CAJCATGACATTGGACAATAGTACTCTTTTCTAC
WI-9413	112 G	---	---	GCCAGTCTCTAGTAAGTCTAGGGACATGACCAGACCAGAAGCCCTGTTCTATATGAAGACAAAC AGGTGGCATACTTGGGTGGAGGATACCGCTGCTATTTCCAGATG/CAAGATTTGGTGGAGGAG ACCATGACAGATGACAAACGGAAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T	---	---	AAAAAGCTTTAAAAAAGGTGGTGTCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCAGCT ACAGCCT/CTGGTGCATCTTAACCCCTCTCCTTTT

WI-9617	37 G T ---				TGCTCTTTTATTTACAGTTTCACAAACACACGCGCTG[G/TTGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGGCGGAAGGTCTCATTTCTGTCCTATGGACTGATGAATTTGGGATGGCCAG CTCCAGAAATGTTCCACGTGGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGTTGCACGATGCAGCTTCAGTGGGTCCAAAGCGGGTGTGCTGTG
WI-9657	121 T G ---				AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTGCTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAG[TTG]ATAATTCCTT TGATTAATAATAATGTTTATAAATGTTTATGAAGCTCATTACATTTATCTTTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTTCATAATTATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C GCTGGGA			AAAAATTAAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]ACACCACACCTGGTTAA TTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTGCCCCGTCTCAAAAAACAAACCAACTAAC
WI-13119a	51 C G ---				CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[G/C]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTGCCCCGTCTCAAAAAACAAACCAACTAA C
WI-13112	71 C T AGCTTTT			TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACAAAAATTTCTAAATATCCTTTAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACACTATGGCAAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36 C A CTCAGTACAA			CAAAGTGTACA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGTGACACTTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCCTTTATCTTCCCTGTGGATGAGATGTGCACACACAAGT AAA
WI-13020a	108 G A CTTT			CTAATAGTGG AACCTGAGA CTTT	TGCTATTTCATGACAGACACGTCAGACAAATATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCTTGAGACTTTA[G/A]ATCTGCAAGGGGTTTAATAAT GCAAAATATCACATATATTTCCATTTTAAACACCATAATTAAGTTTTCATTTCTTAATAGAAAAATGA TAAAAAATGTTTCCCAATAT
WI-12837	87 A G AAAGTCCA			CCATATACAT ATATCAAGGT ATGCTGTTTTT	TGTATAAAAAATCCAACTGTTTCCACAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G]TACAAAAAACACAGGATTTCCATATGGCCAGTGTCTACAGAAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCCAGGATGAGGCCAGAAAGCA AGTTGTGTC

L42611b	50	G C ---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCTGT[G/C]TCTCCTCGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCAGTCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATAATGTATTACCA CTGGAGCTTCACITTTGTAC
L42611	34	T C ---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTT[C/C]CTCAGGTTGCCTGTCTCCTCGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCAGTCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATAATGTATTACCA CTGGAGCTTCACITTTGTAC
WI-1172b	179	C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/C]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A ---				TGAACGTGTGGTTAAAA[C/A]TAGGCAATTTGGTTAAAAATCAATTTAAAAACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A	GCAGATTGGA AGTGTAAGT	CACITTAGATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAGTGTAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTTCAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCACTTAACTCTGCAATTTTGAAGAACTAGATTGAAT TCCITTTGCAAAACCCCTTGCCATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAACATGG CCTGGTG
WI-1231b	141	G A ---				TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAAACATCCCATATTTC CAACTAAGCAGGAGTGTTCACAAATAAACAAACATAGGCTCTTTATCTCCTTCTTCATTAAATTTCTT TCAC[G/A]TTATTCCCTCACCCCTGAACGCCCTTCTCCTCGTAGTGACATTTTAAAAATCCACTTTAC ACATTCCGAGC
WI-1231a	126	T C A	GGCTCTTTATT CTCCTTCTTTG	CGTTCAGGGTG AGGGAATAA		TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAAACATCCCATATTTC CAACTAAGCAGGAGTGTTCACAAATAAACAAACATAGGCTCTTTATCTCCTTCTTCATTAAATTTCTT CTTTCACGTTATCCCTCACCCCTGAACGCCCTTCTCCTCGTAGTGACATTTTAAAAATCCACTTTACA CATTCGGACC
WI-472	114	G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGCC		GAAGGCAGGAGTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACACAGAAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG T TACTCTATTT TGTC	AAATGCCACAG GTGGCT	AAACCACGCAACCTTCAAGCATGCTGTGTTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CTTCCAACT CTACACAATCT T	AGCATCACAGCAGAGTACCTTTTAACTT/CJATAAGATTGTGTAGAGGTGGAAAGGAGGACAGGA CTGTCTGTGGTATAATGACCCGTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAAGCAGAGAGGTTTCAATTGACTCTAACTGAGTAC/TAJCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAG/C/TGAACAGAGAGGTTTCAATTGACTCTAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTCGGCTTCTTCCACAGTCCACATGGGTGCCAAACAATCCACATTCTCT ACATCTCTCCCACTGGGCTGCCTTCCACAACTCACC/A/GIACCTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACCTAGCCG/A/GCTGTGCATGTGGATTAGAATAAAATA AACACAAAAATGAAACACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAGAT AATAACTTCAA
WI-991	37 A T	---	---	TGCATTCAATTATGCACCAATAATACTTCTGTACAT/ATJCATTTATTGTATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACTGACTCTCTTTCTCTCTTTGAAAACAAGGC
WI-1011	70 G C	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATCTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC A/GC/JAGAAAGTCAATTTGTAGGTGTTCTGGGCGTTTTTGTCTACGTTTCCATTTCTCTAATACACTGC CGCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTGTTTTGCTGCACTTCTGCACTGAAG
WI-5381	178 A T	---	---	TTTCATGCAGAAGGTCCATGAGTTACAGAACTCAAGGAAGAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGTCTCATGAAATGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAATCACTCTATCCACGTGCAGAACTGGCAATTAGTTTTGT/ATJTTACTAAAACACAAATGT TTAACTTGGGGTCCACAAACAAAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5791b	76 G A	---	---	CTATGTATTCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCTCTA GAACCTCAG/G/ATCGAAAGGAAGTTTCACTAGTCCATAGACCTTATCTCACTGACCCCAAAAGGTA AAAAATAAATAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTGCCACCCCTGTTTGT TAGGAA

WI-5791a	44 C G ---			---	CTATGATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTT[C/G]ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTATTTTGCCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGGCAA GG
WI-5406a	42 A G ---			---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAG[A/G]GCCACTTCCACAGATGCAACAG GCCTTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATTCTCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTTT TCAAT	---	CCATTCTCTTCTCCTCCCTCTCCCTTATTCTCCTCTGTTTCTTTTG[C/C]ATTGAAAAACTGGTT TTCTAACAGTGTGCTGGTATGATCTATCTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATTC TGATCCGATCT		CCGTGCTAATAATAATTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[A]TAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAATATG GTTTAAG		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG[C/T]CTTAAACCATATTTTTGTTTA GAAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGAGTCG	TGTCATTTATG CTGAGTCG	TTACTCCAGG CTCCAAGTAT		AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCG[A/G] ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29 G A AATTT	CCAATTTTAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTT[G/A]AATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38 T C ---			---	TCATGAGTCTTCTTCAAGATGCTTGTAAAGTCCCA[T/C]CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C ---	CCCAATACCTT TTCAGGTGAA	---	TATTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTCCCTTGATAGTACGCAATGGCCAGTTTATACATATTCTTTAGT[C] TTTCAAATTAAATGCCACCATAGAAATAATTTCTAACCAACGAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTACTCTTTACAC
WI-5546	40	C T A	GGCACCAGCCT TTTTAGAGT	CCTGTATTTTA GCAACATGGG	CCTTATAACCCCAATACTTTTTCAGGTGAAAAAGGGAAAA[C]TACCCCATGTTTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAAATTACAAATGCTTGAGTGTAATTTCTGATGTGGGAAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG OCCAGG	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGAATGAGCGGGTATGGGT GGGGCTATCGGCACCCAGCCTTTTAGAGT[C]TCCCTGGGCAATTTGTGCACCTAGTGTGAGA TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATACTGGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]TCCATTTTGAATAATTAAGCTTTTGAATGTTTTTCCA ATG
WI-5836b	161	C T ---	---	---	TCGGGTATTAGGATCGCTTCAACCTCGATGATGGCGTTTATAAGGAGGTGGGA[C]T]GACAC ATTACTCTCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5573	58	C T	GTTTATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	CAGGACCTTGGAGCCTTGTCTTGTCTTCCACCTCACTCTTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCA[C]T]GCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGTTGG
WI-5850b	134	G A ---	---	---	CAGGACCTTGGAGCCTTGTCTTGTCTTCCACCTCACTCTTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCA[C]T]GCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGTTGG
WI-5850a	92	C T ---	---	---	TGCTGTATTGACACATAGTTATCTGACAGTAAATCATCTAACATCACAAATATCTTATTCTGCCTG TCACACTAATTTGCAAGGATTCAAATTGATTGACTATTAATGAGCATCGTGTCTTCTAT]CAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTTCCGTAACTCAAGTA
WI-5612b	125	A T TTC	CTATTAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAC ACTG	TGCTGATTGACACATAGTTATCTGACAGTAAATCATCTTAACTTAACTTATTTCTGCTGC CTGTACACACTAATTTGCAAGGATTCAAATTGATTGACTATTAATGAGCATCGTGTCTTCTAT]CAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTTCCGTAACTCAAGTA
WI-5612a	44	T A ---	---	---	TGAGAGCCCAATTTTATCCGCAATAAA[A/C]T]TCCCAAGTCCCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGCAAGGTGAGACAGATGTGAAGAAC
WI-5636	26	A C CCGCAATAAA	GCCAAATTTAT CCGCAATAAA	CATCGAGGACT TTGGGA	

WI-5865c	103	C G ---			---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC ACTGACTCACTCACTTGTCTATCAAAAATTAAACG/AAATATTAATATTTTATTTACAGAGGAA CTCAGAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACTAAATAATCCAGG
WI-5865b	99	T A ---			---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC ACTGACTCACTCACTTGTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACTAAATAATCCAGG
WI-5865	165	T A ---			---	TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTTATGCAATC ACTGACTCACTCACTTGTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGTAAJCCAGTCTCCATCTTCAAAAGGTCACAGTCTTC AGAGAAGACAGACAACTAAATAATCCAGG
WI-5874	76	T G	CATAGCATGG ATAATATTAT ACAGAAAAA		CCTAGTAAGTT TCAGTCATTGG ATAATGT	CTCAGACATTCATTTTATTAGTTGTTAAATTTTGTGTATTTCATGATGGATAATATTATACAGAA AAAAAATTTG/TACATATCAATGACTGAAACCTTACTAGGTAGCAATTTGTTTGTCATTTGCT CATGGAGCCGACGTTGAGCTCTCAGTTTTCATCTA/TTTTTTTCAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTCTCGTATTTCAACTCTCATTTGCTGATGGATGATGATCAATAAATGGGTGATTC AGAAAAAAGTAAATG
WI-5752	36	A T	CAGCCTCTCAG TTTTTCCATC		GACAGAAAAAG AGAGTAAAT ATGAAAAA	TTAGCAGAAACAACAAAAAATGTCAACACACTGCAGTAAAGAGTGTTCCTCGATAAATA/C/GJC CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAGCCGAGTTTCGATTACACACA GTTGCTGTTTAACTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGCG/ATCCACGAAA CATTGTTGAAACGAGCCACGTTTTCGATTACACAGTTAGTTGCTGTT
WI-5760b	61	C G ---			---	TTAGCAGAAACAACAAAAAATGTCAACACACTGCAGTAAAGAGTGTTCCTCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAGCCGAGTTTCGATTACACAGTT GTCTGTTTAACTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGCG/ATCCACGAAA ACATTGTTGAAACGAGCCACGTTTTCGATTACACAGTTAGTTGCTGTT
WI-5760	187	G A ---			---	AAATCTGGCCTTTTCTCTTAGGAGGAGATTTCTCACCATGGGAATCTTG/AGT/GCAAGTTAGAT CCACCCCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTTCTCAGICTTCTTGCTG
WI-5944	52	A G	TTCTCACCATG GGAATCTTG		GGTGGGATCT AACTTGCA	GAGTTTAAATGAATCCTGTTCCCTCTCTAAAAACCTCTCTGTTCCCTCCCACTTCAATTCAGCAGATAT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGATTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGTAC/TTTGTCTGTGCGGTATCTGTCTCAATCACCCCATTCACCTTTATTTCTTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148	C T ---			---	

WI-5967	165 C T ---				GAGTTAATGAATCCTGTTCCCTCCTAAACCCCTCCTGTTCCCCCAACTTCACATTCCAGCAGATAATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGTGATCATTTTCAAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGCGGTATC/TJTGCTCCAATCACCCATTCCACTTTATTTCCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ---				GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAGTCCAACTGTGCACAGCCCCATTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACITTCAGCAAACCTTGATTGACGGGTGAC ACACCATGCTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA			GACTCTGCTCAAGAAAAAATAAATGAATAATTGAATAATTAAAGCACITTCCTTAATTAAGCAT CTACAAGGTACTTAT/CJ/CACGTGTTCTGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAAACAGGATTGTTACATGACAGAGAAATAGGGGAGATAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTCACA	CCAATGACTT ATTCTATATCT			ATAGGACAGTTTTTCTCCAATGACTTATCTATATATCTGTACAT/GIAGAAGTACCACACATTTCA AACAAGAGCCAGGCTATGCCAGGGTGGGATTATTTACGGTCATGTAATATGCATGTAAGACTA TTTTACTGGCTTCTTTTATGCATAAAACAAAGGTATGGTCTATTCACAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAATATAGTCTTTATAGAATATGTGTTTGAATAAAGCCACA AATTATCTATAAAACAACA/CJ/TAAGGAACGAGGCTCAAAAGTGGAAACAAAACGGCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-6461	88 C T ---				GAACTATCCTTTAGTGGTGCCACATTTCTATTTCTGATTTCTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTGAGTGAAGTATGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTTGT CCTGG/G/AJAATATCTCACAATAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466c	141 G A TTGTCTGG	TTTTCACAGTC			GAACTATCCTTTAGTGGTGCCACATTTCTATTTCTGATTTCTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT/JATTCAGTGAAGTATGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT TGCTCTGGGAATATCTCACAATAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCTTT
WI-7466b	80 T C GTC	GACTTTCTGGG CTATGAAATA			TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCTGTCTCCATTTGCCACGTCTCCTC AGTAGAATAAGACAGGACTTTGCTGGCTGCTATCTC/AJTTCTCTCAGAGAGCAGCTTGGCCCT CATAGGCATTCATAGATAATTGTTGAATGAATGTGCTTTTTCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104 C A ---				CCCTTAACAAGAAAAACTTGACTTCTCCTCAACTCAAAATACCCCTTCTCTAATAATTTA/GJAGTAACCA AAATATTCCTTCAATAAATAATCTTTTAATTAGAAGAACGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9720b	55 A/G ---				

WI-9720a	47	A G	---			CCTCTAACAGAAACTTGACTTCCTCAACTCAAATACCCCTCTCT/AGJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123	A T	---			CACGCTTAAGGCAGGATGGCTTATGAGATACITTTGCATTGCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTCT/ATJGAGGATTAG TAAGATCTCTTCTAAGACAGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTTGCATT TAAGATTGCCAGTCTTTTGCCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C G	---			CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTCTAAITTTTATATGTTTACCCTTT GTCATT/CGJTCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCCA
WI-9943	91	T C	---			TGAGGCTATGATGCAGATTTGTAGTACTAATCTTATTAGCAATTTCAATGTTGTGGGCACTGTT CGTTGTGTTTATATCCATCTCT/ICJATTTTAAITTTCTACTGAGCAGAAAAAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTTAAATATGTCATTACACCTTCTCTTTTGTCTTTAGGGA
WI-9891	39	T C	---			AGGGGCTTCACAGATCCGTAGCTCAACACTGCCTCTT/ICJAGTGAGCTGTGAACCCACCAAGAC GGCTGGTCATCAGTGTCATCTCTCTTTCCTTTCCGGACAATCTTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCCAAATATCTTGTTTTAAATCTCTTATTAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCATCTACACAAAAAGGATTGCAAA
WI-9897b	84	C T	---			CTCAGAATTATTCAGATCTTCCCAAAATGTCATGATCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/ICJAGTGCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A T	---			CTCAGAATTATTCAGATCTTCCCAAAATGTCATGATCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/ATJCAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115	C A	---			AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTCTTATGGGTGCTTGGACTGGCAGGGGAGTTAGACA/ICJAGCCAAAGAAAGGCC TGATATTAAAGAGGCATTCATTAA
WI-9935a	42	C T	---			AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTCACACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGAGTTAGACA/ICJAGCCAAAGAAAGGCC TGATATTAAAGAGGCATTCATTAA
WI-9983	146	C T	---			CCTGTTAGGTGGCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCTCCCATTTCTCTTCTTGA TTCCCCAAACCCAAAGGTTCTACCCAATCTGATCAATGCTGACTAGGTCATGGCTGGTCAGGGTAA AGCATTATGA/ICJAGACACAAAGACAAAGAGGTTAAAGTGTCTGCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTTGTATTATTTATGTGCTATAAATCAATGGTTCTA ACATTCAAATAGATCTTTTGTCTCTGCTCAGATGCTTCAATGATGTAATGCTATGTAGCAAAT CTA/A/T/TTCCCTTAAGCACAGTAATCAAGGCCTTCTACCCCA
WI-10020b	122	T A	GGGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCTATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTTT/A/AAAAATACC AGACTAATGATTAAATAAATAAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10020a	39	T C	TGTCATCTTGA CTCGTATTAA ATAAATT	AAATCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCTATCTTGACTCGTATTAAATAAATTAT/C/JGTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTTATGGCGAGAAAAGAAATCATGACTTTTTTAAAAATACC AGACTAATGATTAAATAAATAAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGCTAGTAGCCCT CCTTAGA
WI-10064b	170	C T	CCTTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTTAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG/C/JGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C A	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGC/AJATTATAATA AATATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTTAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T C	TCTCCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCACAAACTCTTA/C/JTTAAATCCATTCAATACAACAAGAAATTTATAGAA TATGCCACCATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T	TGGCCTTAG AACATAGTTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTTTATTTA/JACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGTCTGTTTATAAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAACTTAACACTGGTCAGATGTTTAAACCTTGTGAACCTGCAGC
WI-10316	104	T C	CTGTTGATTTT CTACCTCTATT CTGCT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACTTAGTGAGGTGTAATCAGAAGCATCTATATTACCAGTCAACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTTTA/C/JTAAACTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T	---	---	AGTGAGTTGTGCACAATTTGGAGACATTCTGTGACCCCAACTTAAACACTTCTCCACAC/C/JTAC AAAGTTAACACTTCAGTTACCAAGGTGATGATTGAGCAGA

WI-10368	31 C T	TGAAGGAACC AGGCTTGTT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAAGGCTTGTTC/TCTACCCCTCTTAGAGAATAAATAATATCTT GAGATAGGAGGAGGAGCAGCTGAGGACAGTCTGGTTTGTCTACCCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTTCAGGG T
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGCTCAGGTATGACTCCCA/GTCAACTTCTTGACTCTACTCCCATCTCGGTG TCTGCTCCCAAGGGAGCATCTGACACAGCCTTTTGCTTGTGTGACAAACAGAACATTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA	TGCGGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATAATTATCTTTTTCATATT TTCCAAATTATTAATACTAGAAATTTTCCCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATAGCAATGCTGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-10567b	82 A C	---	---	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATAATTATCTTTTTCATATT TTCCAAATTATTAATACTAGAAATTTTCCCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTAATAGCAATGCTGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-10567a	60 T C	GGGTGCTCAAT AAATATTATT CTTT	AAATTTCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATAATTATCTTTTTCATATT ATTTCCAAATTATTAATACTAGAAATTTTCCCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAATGCTGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-11153b	84 C G	CAAACTTCAA ATTGCTTTAAG TACTTTA	AAATCCAAACA GTCAAGGTCTT C	CGTTGGGAATATTCTATCTCACCTAAATTAATGCGGTGATTAAATATACATTTTAAACAACTTCAA TTGCTTTAAGTACTTTA/C/GTGAAGACCTTGACTGTTGGATTTTGTGATTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTCTATCTCACCTAAATTAATG/C/AJGTGATTAAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGTGATTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAAATTG ATCC	CCATGGCTGTA GTCCAGT	GTGTGAAACTCCAGTATCTTCCCTCAAAACCAAGCTTAAATCACAATCAGCTTTTCTTCTGTA GAGCTCAAACTCAGTCTGAATGAAATGCTGCACAAATGTAACAAGAAATGATCCTA/T/C/ACTGGG ACTACAGCCATGGAGAAAAGCAATGTATGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGTCTCTTICA TTTGAGGTTTT T	TGACTCAAGGAACACACACAAAAAGTTTCAACCAAGTGAATATGACCAAAATGAGA/C/T/AAAT TTGTTAAAAAAACCTCAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTTGT ACCTACAAAAATAGGATAGTCTGTTGGCAGACTTTTCTTTTCTTTTCTTTTGT/GJCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTTCCCTCTCCCCATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCAGGTTCTGCTCTTCCCAATCCAGAGGAGGTACTATTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGMAAAC
WI-10656	59 T G	---	---	---

WI-11169b	154	T G T T T T	TTAACCAAGA G T T T T C A T T C	CTA A C T T A A A A A T C C T C A T T C A A A A T A T A A	CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACCTTGAAAAAATAAATTTAAGCCTAAAGTAGTGCCTTTTAAACCAAGAGTTTTCATCTCTTTT TTTAAAAAAGAGCAGACAGACAT/GJTATCATGTGTTCTGATAAATTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A G T T G A A A A	AATAAGTGAA AGTAAGTAC	AAACTCTGGT T A A A A A G C A C T A C T T	CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACCTTGAAAAAATAAATTTAAGCCT/GJAAGTAGTGCCTTTTAAACCAAGAGTTTTCATCTCT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G ---		...	CAAGTGTGGACCTTGGATAGGTG/GJACCGGCTGAAGTTGGACAGTTGTGGTTAGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTGTTCCTTTTGGGTTTACCAGTGGGTCACATAAG AGAGATGGGAGACAGTCTCAATCTTGCTAAATAATCCAAATAGCCATGGTTTGGACAAAATAC AAGGTTAGTGTCTCTAATCTTAATGGGCATA
WI-10686	133	C T A A G G	TGCCCCGTGC T A A G G	CAATCTCTAAA T T C A T G T G T A G A C A C A	AATAACCTGTGGACATAGGCAATACTGAGCCCCATACAGAGTGTATTTATGTTAATATTGAAA AAAGTCAAGAGAAAGATGATATAGTTCTGTAGAACTCTGAAATCTGATGCCCTGTCCAAGG C/TJTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG
WI-11175	77	T A A	AAATGATCTT TCTGCTCAAAG	CTGTTCTACA T T C T T T T T G A A A A	GGTAGGATGATTTAGAAATGCCACTTACAGCCACTGAAATATATTGCCCTCCAAATGATCTTCTG CTCAAGAGAGT/AJT T T T T T A A G T T A C T A T T A T T A T T C T G C T T T T C A A A A G A A T G T G A G A ACAGTACAAAATGTGTTTCAAGTATAGCAAAATTAATTAATAAGTAAGAAAAAGCAAAAT TGGG
WI-10694	144	A G T A T G A G T T T C	TGCAATGCTT T A T G A G T T T C	GGCATTITGTA A A G G A G G A A	TAGAGAGGCTTTCAGTTTCAGGGTTGGAGGGTGGTGAGGTGAGATTCACCTTCTAGAAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAGAACTCAGTTCTAAAGTGTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTCCTCTCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT T
WI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTCTC T C T T G T G T C A T T C	GTGAATTCATCCAGAAAAACAGT/CJGAATGACAACAAGAGAGAAAAAGAGATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGCCAGTGCATGGAGCAGTG
WI-10719	115	T C G C C A T T C T A G	TGACTCTCAAG C G C C A T T C T A G	GCACTGCCAGC A G C C	CAGGCCCAACTCTGTCTAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAAGTTCTCTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCATAACTAA
WI-10721	40	A G C T T G C C A	TGGCTCTGCTA C T T G C C A	GAACTCCAC A T A A A T A A A T C T C A	CAACCAATTCAGATTAAATTTTGGCTCTGCTACTTGCCCA/GJATGAGATTATTTATGTGGGAGTT TCTGAAGATCCATGGTAAATAGTATCTCTCCCTGCTAGGTTTGAAGAAGTTGAA

WI-11204b	88	T C	---			GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACCTTACACCTTTT[C]ATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATATTTCAGAAG GCAACATC
WI-11204a	80	T A	A A C T T			GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACCTTT[A]CACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATATTTCAGAAG GCAACATC
WI-10732	80	C A	A T T G G T C A C T			ACATGTATTTCCCTTTAGTGGTCAGCCCTCCCTACCCCAAGAAATATCCCTGGTTTATTGCTGTCTTC ATTGGTTCACCT[C]ATTAAGTTCTGTATGCATTTGTTCTTGAGTCCACATAGGTGTTAATCATTCOA CACCACCTCTGTTTAAACTGTC
WI-11206	127	A T	A C T C			TAGTCTTTTCTTTGTACGAGTGTCTATAAAGAAATTACCACCTCTGCACATTTTGTAAAGATAGCACAG AGAGAAGCATTACAGGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTC[A]TCCAA CCATTAGGATTGTCACTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATCCACACATGGA ATAAGTCTA
WI-11215	68	C T	---			GAAAAAAGTTTTAATGGATTGCTTAGTTTGCTTAAATTTGACCTACTTTTCTGAGATTTATTTTAGT [C]TATTTTCTATAATATTTCTTGTAGTGATGGATTTCTATAAATTAAGGAAACAGATAATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTATCCAAAGCCCATTTCCACCATGT TTT
WI-11219b	89	G A	A G A G A A A			ATGAAAAATGCATTAGAAGAAATGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]JAGAAAGTGTAGAAAAATTAGAGGCCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18	G A	---			ATGAAAAATGCATTAGAA[G/A]AATTTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGCCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136	G A	G C T G G			AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAATGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGGCTG G[G/A]TCACAACITGGCTACAGGAGAAACCTGCACACAGACTTCGTAATTTGCTTTTCACAGGCTACTGG AAAGCC

WI-11222a	25 C T A	GOACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTGG	AGCCACAGTGAATCATTTACACTA[C/T]CGAAATCAGCAAATGCTAAAATTTGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCGTTGAACATATTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTACAACTTGGCTACCAGGAGAACTGACACAGACTTCGTAATTGCTTTCACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATGCCATATTAAATTCATTACACTC[C/T]ACATCATATTTTCTTAGCAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCTGGCAGCATATCAATTTGTTATCATTTAGACATTGCA GGAACCACTATGGATGATAAATGTGTGTTTAAATGAAGCAAGCAATTA TTGCATGCAATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAAATGTGCAAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATCCACAAAATTAT TTCATGA
WI-11226	165 A C ---		---	CAGTGGCTGGTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTCACAGCAGGGCCAGGAAGGTTGATCTGGAG TGGACACACTGCTCTAGACC[C/T]TCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCOCTGGGACGACAGGATCAGGGCCCTAGTCTCTCTGGGACAGTGAAAGGGCCACCAAC ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGAGAAAGCATCTTCATGGCAGGAATTC[T/C]CATTT CTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAAAGAGAAATGATGA GGACCAACAGAAATTACTTGGCA[T/C]JAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATTTTGGATACATTAGGCTCATTTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10778	62 A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	TATGCCCTCCCAACGAGCATCCACGCTGCTCTTAGCAGAAAAAATAGAAATACATCTTCTGAATG GGCACATTAATCTGCAGGCTCTCC[C/G]CJTTCCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGGAGGATGAGAGAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	GAATTTAGTATTATCAAAATTTGCCAAAGACCATTAACAAGATTAAATAGTTAAAGCCAAAACTATA AAGAATTAACGTGTTCAAAAGTGTGTTAA[T/C]TCTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT GGATGATGTTCTGTGGTCCCTTTA[T/C]JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGATTTCTCGCTACCCATAGTCACTGCTCAAGTGTCCACCCCT
WI-10810	58 C T GCAGGAAT	CATCTTCATGG GCAGGAAT	CAAACCCCTAAG AAACACAGAA ATG	GGATGATGTTCTGTGGTCCCTTTA[T/C]JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGATTTCTCGCTACCCATAGTCACTGCTCAAGTGTCCACCCCT
WI-10828	23 T C ---		---	GGATGATGTTCTGTGGTCCCTTTA[T/C]JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGATTTCTCGCTACCCATAGTCACTGCTCAAGTGTCCACCCCT
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	GGATGATGTTCTGTGGTCCCTTTA[T/C]JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGATTTCTCGCTACCCATAGTCACTGCTCAAGTGTCCACCCCT
WI-10834	96 C T GTGTTAAT	AGAAATTAAC GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GGATGATGTTCTGTGGTCCCTTTA[T/C]JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGATTTCTCGCTACCCATAGTCACTGCTCAAGTGTCCACCCCT
WI-2287	24 T C ---		---	GGATGATGTTCTGTGGTCCCTTTA[T/C]JAAAGCCCTCTTGATCCCAATGTGTAAATTTATTTATCT TGATTTCTCGCTACCCATAGTCACTGCTCAAGTGTCCACCCCT

WI-2296	81 A	G A	TGTTACTTTGA TTCCTTGCTCT	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGTGGCATCTAGAAAGGCTCAGGCTTTAGAAATGATTGTTACTTTGA TTCCTTGCTCTGAC[A/G]CCAGTAGCTGTGATTGAGAAAGTTACATTTGTTTGTG
WI-2300	77 G	T C	GGCAGAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTATTTAGCGGGGCGAGGTGAGGCACAGAAGC CAGTCATAC[G/T]GCTTTAAATTTGACCCCAACCATTAAGAAATAGCATTTCA
WI-2371	55 G	T C	GTCTTGTTCTT CCCAGCTTCT	CAAGATTGAC AGCCACCAC	CAATGATCCCCAACATTTCCAGGGAAGTCTGGTCTTGTCTCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTCCTTGTCTTGACGTGTATAATCCAACTCCTTGCTCCAGCTTTACATGATGT TCTCTCGTGTCTGTG
WI-2395	122 A	C T	GAACATAATT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAGAGATAACATAGAATATCATAATAACTTGGTTTAC TGAAATCTGAAAACCTTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCCAA[A/C]CTGAATTC AGAATAAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATATTAGTAACAAATCTTTA CATTTACACAAACCCCA
WI-2437c	192 G	A ---		---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGAGCGCATTATG
WI-2437b	179 G	A ---		---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGAGCGCATTATG
WI-2437a	128 G	A ---		---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGAGCGCATTATG
WI-2440	71 G	A TTTTAGTT	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCGAGAACT
WI-1356	123 T	C GAAAAA	TGTTTAGGAA ATAATGACAA	TGGTTACAACT GTACCAAAACAT G	CTGTAACCTTACACACATCCTCCTGTAACTCTAGGTTACTTGTAAATACAAAACACAAATGTAATGCT ACATAAATAATTGTCATACATATTGTTTAGGAAATAATGACAAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCCCAATATTTCAATCCACAGTTGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C	A GGGAGAAGA	CAGAGTCTGG	TTGCCATGCTT TATCTGTT	ACAGTTAAGAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAAG[A/C]AAGCAGATAAAGCATG GCAAAGACCACGCTGAAGATATCCAGGGTGTGTATGTGCACATAGGAAGATCATTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAGGTGTGAGAAAGAAACAGAGGCGGTT

WI-3416	33 C T	CCAAGTTGTA GCAATCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCAAAGTTGTAGCATTTCAGAAAGTC C TCTCTTAGAGGTAGTTGTGCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCCTCCAAACAAGTGTAACAACAGCATTGTTAAG GAAATGTGAATGCTTGTCTACCTCTGAGGCACACAATAATTAATCCCATTCCTTAAAGACACAGG
WI-3453	70 C T	TTCTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAACAAGAAAATTTAAACAAATTTGAAATCAGCTACTCTTCTTAGGCCCATCAGAG AATC TGAAGTCATGGGAAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGACACAATCCCACTTCAGAGCCATCATCTGTAAGAC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC A G G TATTTTAAATGAGTGGTGTGGGAGAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC A G G TATTTTAAATGAGTGGTGTGGGAGAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGTTTCT GGATGCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCCATAAGAAATGGTGGAAAAATAAACGGGAGAGAACCTGGG TTTCTGGATGCT C T T GAGGACAGGGTCAACCCAC
WI-3600b	146 G C	GGTTCTAAC TGGATATAA	OCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGGATA TAAACATCT G C ATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTCTGCCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT G G GAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3678	125 G T	---	---	TAAATCATGCTTATTTTCACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTGTTATGATGCACCT G T CC TTTGG ATAGATGTTGTAGGAGATGGTTGTTAAAGACACAATTTACCTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTGTAATCACTGAATGAGTTCCAAAGCCTTTATGCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCAATCCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T A C J AAAACTACTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAATGCTACTTAAACAGG ATTCTCAATTCATCCAGAATACCTCTGTCTGTCATCTTAACTTTGACTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA	GGCTCACCAAT CATTTT	TCTAAATGTGAAACCAAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAATGA AAAACT C J ACACCGTTTCAATGAAAAACAATGATTTGGTGGCCCATGTCCCTTATTTAATGAAAA GATCTTGGCAATTAACCT

WI-1819	51	C T	---			GAAAAAGCAGGAAGCCAGGAGGACAAACATTTTGA AAAAGTCTTTCAGCACIC/TJTCGTGGATCCG AATTTAGTGTGATTTGGCAGGCAATCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAAATGAAATGTGGA AAAA AAAA AAGGGTGGTAAC TGT AAGCCTGCTGCAATGTTTAGACACAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	---			GGCCTATTACATGACACTGGCCCAAGATCTTGCTCCCTTTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTGCG/A/GCCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	C A A	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGTGACAA/T/CJGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAAGACACAGT CATTAAAGTGGAGAAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA	TCGTGGTGTG CTCTCC	CAATGACCAATGTCTTTAGAAAGCAG/A/CJGGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGAGCCACAAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT
WI-3901	114	A G	---			GGACCAATGTCCTCAGAAAGTACATTCAGCCCTGGACGGTGTCTCCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAAACCTCGGCTTCTCACCTGACAAGTGG/A/GJTATCATGTGCTACACTGC AGTGTTTAATGCTGCAT
WI-3914	99	C T	GC	TGATTTCTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAACCTTTTATTACCTCCCTGAGTTGTTGCCCTTGCAA GACATTGCTGATTTCTCAAGACTCACAGC/C/TJACCATCCTTCACTTGTCTTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCCTATGAATCAT/G/A/CATTTGTTCTCTGTTATTGCTGTTACACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTATAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	T	GC	TTGAGGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAA ATTGTT	TAATTCACATTGCTCTGTTTGTGCAATTTATGCTTCTCTTATGTAAACACAAATCACCAACATTGAGG TCTTAGTCATTGCATG/A/TJGTATAACAATATTGTCACCTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGAGGTAGGTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTGTCTCTATAATTTAGCAACAATATCAACAGAA/A/GJGGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTCTCTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA/A/GJCTGAAAAATCTGTTGGCAATCTATTAAAGG CAATATATACCAGCAGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68	T C	TACCTA	TGAATAAGCA CGTATTAAATT	AAGGCAGCAA ATCATGATG	ATGCTGCGATACACTTCCAAATGACTAGTATGAATAAGCAGTATTAAATTTACCTATTATATT ATTCATTAAACCAATAG
WI-4199	51	A C	AAAA	CTCCCCAAGTT AGTCAATATA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCCAAGTTAGTCAATATAAAAAA/C/CACACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24	C T	CTGCCTGT	CTGTCACTGGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGCTCACTGCTGCCCTGT/C/TTGGTCTGTTCTCTGTTCTTCAATGTTCAACTGCTTGAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGCAT
WI-4250b	117	A G	---	---	---	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACACAGGGTGGGAAGGATCCTGTAAAGG/A/GJTAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94	G T	AGG	TCAATATGAG TCTTGTGAAC	CTTTTACAGGA TCTTCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAACACAGG/G/TTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68	G C	CACCT	TGCTCCCCCAT	G	TAAATGCTCTGGGAGATAATAGGAAGGTCCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT [G/C]CTTACACAACTTGAAGTAGGCCCCATCCAAACACTGGTCAAGAGATACTACTGTCGAC
WI-4256	57	C T	---	---	---	ACAGCCTCTTCAAATGGCACAAATCAAAAGCACCCAGTAAAGAGAGGCAAAATCTGG[C/T]CTCAC CATTGGAAAAGTCTTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
WI-4325b	71	C T	---	---	---	AGTTCACTGCCTAGATGAGTAGACCATTGTTGCTTTTAAATGTACATGGGACGACCCGGAATGG GATG[C/T]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C T	---	---	---	AGTTCACTGCCTAGATGAGTAGACCATTGTTGCTTTTAAATGTACATGGGACGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4347	158	A G	---	---	---	TGGGCAAGTCCGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCTGTCACCTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCACCTCCAGCCAG GGCCTGTATCTGTTCAAGGCC[C/A/G]GAATCGTCACGGCTCACAACTGTGGAGGTAGGAATGACGA G
WI-1936	117	T C	---	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCTGGTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACAAACCCAGTGGGACACAGGGGTACTTGTATACCT/C/CTCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCTTACTTCCACTTGAGAAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGGA

WI-5204	54 C T ...		---		TAGATTTTGAATGATGACAAATAGGGAAGCCTTTGTTAAATTTGGGTTTGAAGAA[C/T]GAAGAAAAA TGGAAAGGGAAGAAATGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCAGTTTGAAGTGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAAACAGA	AGATAATTTTG TAAAGATAGTT TTGGC		TTTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAAATATTTAACAGACTCAAAAA TAT/G/GJGCGGAAAACATCTTTACAAAAATATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCCT GTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAI
WI-4448	112 T G A T A T A A	TTGTATCAAA GAGATGGGGT	AATTAAGAA ATCTTTACATG GTTCTTT		CCCTGAAATGTGCTTGTCTCTCCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTTAAATTAACITGTATCAAGAGATGGGTATATAAT/G/JAAAGAAACCATGTAAAGATTT CTTTAATTAGTGAATTCATCAGGGCTCTCCACTGCTATCAGTAAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAAT	TTTCCTGTTAT GCATGAACCTG		ACACATTTTCATTTTGGCTTTAAGTTGAATTAATTCAGAAAAATATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAAACACCAGGTGGGGCAATTGATTGAATTGT
WI-4461	49 A G C C T T C	TCACTGTTATT TTAAAAATTAT	TTTGACCTTTC ACCAATTTCA		CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAAATATCCCTCC[A/G]TGAAATTTGGTGAAA GGTCAAGAAATGAATCCCACTTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75 G A ...		---		CTACTGGATTTACTTTGCTCAAGCCAGACACACGAAAGT[A/G]TATAAAGAAACAGTTAGTAAT TCACCTTT[G/A]TATTCTCTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAACTGTTT TCCTT		CTACTGGATTTACTTTGCTCAAGCCAGACACACGAAAGT[A/G]TATAAAGAAACAGTTAGTAAT CTTTACCTTTGTATTCTCTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA		GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCATAAATGGCAGTGCACAGGTAAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAATAAA GGAGTGAATAAATGAATGCCATAAT[C/T]CTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T G A G T	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCTTIG		GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAATTCAAACCATAAATGGCAGTGCACAGGTAAACCA GTGGTGAGATGCTCTGAGTT[G/J]CAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCATTTCTG	TTCTAAAAATA ACACTTCCTGA AAAA		TGAGAGAGTTTTTGGATTATTCATCTCTGCAACACTCCAAGTAAGTCTATCTGAAGATG[T/C] GAGTCTCTTTTATATCTCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAAGTCTCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTGGTGGACAAAGATGGCCCTAGGATCATTTT

WI-4540	110	A G	GCACATGTGG CATCC	GACAAATGCAGC CATGCA	AGCTTTCCCTTTCTTAAATAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCATGGCTGCATTGTCCAGTC AAATGAGACAACCTTCCAT
WI-4582	226	T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGCCAGTTTAACTTATTCCTGTACACA AATAACTTTATGGGAGACAGCATTGTAATCAATCAATCAATGACTCGGTTGGCTGTACAAGCAT AAACAGACGCTTGCAAAATATGGTT[C]CCTCCTTGCTAGAAACCATTTGAT
WI-1965	105	G C	AG	GAATGGATGGG TCATCTCTCT	CAAGGTTAGTTAACTTGGGGGCAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG[G/C]AGAGAGATGACCCATCCATTCCTGG GCTTCTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99	C T	TTG	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAACCACATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAATTAACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG[C/T]CTTTTTCCTTCTCTCTCTCTCTCTCTCTCTCTG CCCTCTTTAACTATT
WI-5248a	38	G C	CTACGTTGT	TTTTAATTTTC TGGGGTGTCT	TGTTTAAACCACATACAGTTTGCTGCTACGTTGTAGAGCAACCCAGAAAATTAACGCCTAC TACCACTTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTTCCTTCTCTCTCTCTCTCTCTCTCTG CCCTCTTTAACTATT
WI-4596	69	T A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTCTCGGTGACATTACTCTGTTGACTTTGCTCTGAAGCAGAAAGCACTGTGA CTT[A/C]ATTATTAGGCCCATCTCTGCTGAAGCCTGCTACAGCAATTTGTAAACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTGACAAGATTCTCTTTTAAACAA
WI-5252	119	A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAGAAAGCTTGGGAAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGCCCT
WI-4606	61	A G	CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCCTA[A/G]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTCTGTGCTAATTAAGTCCCTATTCA ATTACCACTTATCGGGGTAATTAACACTGGAAAGTATGCCAGGCTAATTTGTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77	C A	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAGAGG[C/A]CTTTCATCTGCCCTGGTGGTTTTTCAGTAACTGCAACATGCTTTTGCCTCC CGGATGAAAAGATACCCCTCTATGACTCAGCAATCCACTCTAGGTATGCACCCTAAACATGGGTG GCAAAAT
WI-4649	50	C T	TTCCGAATG	TGACTAGGTG TACTTACAAGA AATCATC	TCACTGTTTAGAAATTTCTCTCCTCAGTGAGACCATTCTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACTCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGATTTTTTAA AAATCCTCCCAATATTG

WI-4650	148	A G G T C T T	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTAATTGTTGTGTAATTTCTGGAGAGTCAGTTACTCTCAGTAGATCATAAAGGG GACTTTGGAAACCAAGATATCTCAAGACATTTAATCTAGAGCAGCAAGAAAGTATAAGTTGTCTC TTATATTGCTTTTJAGJCCAAATCCAGTTTAAACCTTCAGTAAACGTT
WI-4677	82	T C A A A	TCCAAAAGTG ATTAGGTGAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGT/CJAAGTTGAATAATGACACTGTTGAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGACTAGAACACACAGCGGTTTATAGGGGAATACTCAT
WI-4698	135	C G ---		---	ATGATGCTATCATGAGGAATCTGTAGAAAATTTTACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTTACGGAAAGAACTTCAAJ C/GJTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G A A A C C C A C A C	TGCACTATGG AACACCACAC	AATATGGAATC TGCACTTCAAGTT G	CTTCCCATTCTGCCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCACATATGGAACACCACAC[G/AJCAACTGAATGCAGATTCATATTTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C A ---		---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAACAGAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAAGTAAATCACCTTTTGATGTTGAGATTTTCCAGAAACGTGAAATTTAGTAAACCATGGG TCAACTATGAT/CJAJCCAAACAGCAGTGTTGTCTAAAAAATATGATAGTTTCTCTCTCTGTCACC GCAATGAAAAGGAGTT
WI-2028	176	T C C T G T C A T C	TGTTTACGTTT GAA	GGTTGGAAACT CAAAATTACCTA GAA	GACTACAGCGCACAGACAGGCGATTGTGGCTTGCACAGGTGTTGGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGCGCTCTTCAGTTTACTACAGACCCTCATCATCTCCTGGTTCTTG CACCCAGTCCACTTACCTGTTTACGTTCCCTGCTCATCT/CJTCTAGGTAATTTGAGTTTCCCAACC TGTTGG
WI-2033	183	T C A	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAATATAGTATTTCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAGGTTATACAGGACCAGTGTGGAAATTT AGCAATTTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA/T/CJGGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T C ---		---	TTATGGATACATGTTTCTGTGGAGGACAAGAGTTGAAGCAAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCAACAGGCTCCTTCCACCATTCCTCCACTCTTCTACTCTGAT/CJ AGGCAGACTTATATGGAAAAAGGGA
WI-2034	150	T T C C A A G G A C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGGCAAGA CCTCCTTCTCGGTTTTCAGTGAAGACGATGAACCTCTTCACTCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAC/T/CJGGACCTGCACCTATCTTTACCCCTTCCGACACCAAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TG T G C T T T A A A G T G T G T A A G T A T T A A T T A G	A T T T C C T C T T G A A G A A A C A T C A	T C A G G T G A C A A G A A A A G T C A C A T T T C T T C A A T C A C T C A C C A T T G T C T G T T A T T G T C T C T T G C A G T G T A T C C A A G G A T G T C A C T T T T G G A A C T C T G T A G A T C A G A A A A A C T G T C T T T A A A G T G T G T A A G T A T T A A T T A G A T T C T A T T T T G A T A C T T G A T G T T C T T C A A G A G G A A A T T T G T G T A A G A G G A T T C C C A T T T G C A T T T C C A T T G G C
WI-4782	113	C T	G A T G C A G A A G A T A A C T A G A A A A T G C	G A A C T C T T C T G G T T A T T T T T C T G T T C	T C A T T G A C T T T T A G A G T C C T C A G T C T T A T T G T C T T A T T T C T T A G G A A A A A C T A G G C T A G G A G A A C A C A A T T C A G G T C T C C A G A T G C A G A A G A T A A C T A G A A A T G C T G A A C A G A A A A A A A C C A G A A G A T T C A T T A T G T T T T T C C A G A A C G A T T A C
WI-4788	65	A G	G C A T A G A A T C A T C T T G C T A A G T T C C	G G A T A A A A T T A A A A T T T T G G C A T A A	A G G A G A G T T T T G G C T C T T T C C G G A C T C T T G G A A T T C A G T G C A T A G A A T C A T C T T G C T A A G T T C C A G J T G A A A A A A A A T T A T G C C A A A A T T T A A T T T A T C C A A A C T T T A A G T C G A G A T T A A T T G A T A T T A A A A A C T A T A T T G A G T C T T C T A A A A G A T G G C G T A C A C T C T A
WI-5300	38	T C	T C C A G A G A C C A C T T C A T T C	C T A C T C T T T C T A T T T C A T A A T C C A A A A	C T T A C T C C A A A G T T T T C C C A G A G A C C A C T T C A T T C T T C J T T T T T G G A T T A T G A A A T A G A A A G A G T A G G T G T A T T A T T C C T C T T T A C C A A G G T G A A A T T G A G G C T C A G A G A C A A G G T A G A T G A T G A G C C C A A G G T C A G T G A C A G A G C C A
WI-4818b	121	G T	T G A T A A T G G G G C C C T G T T	C C T C C T T T T A T A T G T A T G C C A G A	T A T A A T G T T T T G T T C C A T A G T T G C C A T A G A C T A G G T T A T G T C C A C A C A T G A A T A A C A A T C T T A T A A T A A T T A T T C A A G A A G A A A T A T A C A T A T G G G T G A T A A T G G G C C C T G T T G T C T G G C A T A C A T A T A A A G G A A G G C T A A
WI-4818a	43	A G C	T T G C C A T A G A C T A G G T T A T G T C A G C	C A T A T G T A T A T T T C C T T C T G A A T A A A T T	T A T A A T G T T T T G T T C C A T A G T T G C C A T A G A C T A G T T A T G T C C A G A C A T G A A T A A C A A T C T T A T A T A A T A A T T A T T C A A G A A G G A A A T A T A C A T A T G G G T G A T A A T G G G C C C T G T T G T C T G G C A T A C A T A T A A A G G A A G G C T A A
WI-5317	139	T C	T T C C A T T C T G G T A G C A G T	G A T G C A A A G A A G A A A T G A G T C C	T T T T C C A T T T T G T T G A T T C T T T T G T C T G A G C C C T A G A T C T C C T T A A A T T A A T A G C A A G G T T A A T A A T A T A A T A T A T A T A T A T A T A C A A T T C A A C T C A A C A G G A A T T C C A T T T C T G T A G C A G G T A T A T C T G G A C T C A T T T C T T T G C A T C T A T T T C T A G G T T A T T T G C A G C C C C G A G A T C T A C C C A G G
WI-4888	56	G A	G C A A G A T A T A A A G A T T A A G A A A A G A T A A C A	C A A T T C C A C T A C C T C A T T T A T T C A	A A A T G A G T A A C C C A A G T T A C T C G G C A A G A T A T A A G A T T A A G A A A A G A T A A C A A G A G A T G A J A T G A A T A A A T G A G G T A G T G G A A T T G C T T G A T A A C T G G A G T A G T G C C T T
WI-5328	44	A G	---	---	A A C A T T T T T A A C C A T G C T A C A T T T A C A A C A C A C T G A A A A G A C A G A G A A A A A A A A A A A T A T T T T G C C T C A A A A A A G C T T T A A G A G A T T A T G T A T A A A A G A A A A A A T A T G A A T C A G A A A A A A G G A A A A A A T A G A A A C A C G T G A T A C T G G A A G G A G
WI-4897	93	A G	---	---	G C C T T T T G A G T T T A A G C T T T T T G A G T G T C T T T T T T C C C C C A C T A G G T A C T C T C G G C C C A A A T C C C C A A A A G A A A A A A A G C G C T T G G A G A T A A C A C A T C T T C
WI-5345	29	G A	---	---	C C C T G C T A T A G G T C A G T T T T A A A A A T C C T G A C C T G C T A T G G T T G C T T G T T G A A G C C A C A T C C A C T G A G G T A T A T T C T G T C G C A T T T C T A T A T A C A C T C A G C T T C A G A T C C A C T C C A T C C A A C T T G C A G

Accession	Position	Sequence	Accession	Position	Sequence
WI-5370	143 T C	AATAAGATGG TACCTTAACTA CAGAGAAATTC AAA	WI-5370	143 T C	ATAAACAAATC ATGAAATTCCT GTACCAACITTC GCTTTTC
WI-9711b	423 T A	---	WI-9711b	423 T A	---
WI-9711a	390 C A	---	WI-9711a	390 C A	---
WI-9702c	345 G A	---	WI-9702c	345 G A	---
WI-9702b	344 C T	---	WI-9702b	344 C T	---
WI-9702a	179 C T	---	WI-9702a	179 C T	---
TIGR- A003N21	49 C A	---	TIGR- A003N21	49 C A	---
TIGR- A004V30	203 C T	---	TIGR- A004V30	203 C T	---

TIGR- A004W22	232 C A ---	---	---	GGATAAATCAGTACAAATATGGGGACCTTAAACTGCTGTGATGCAGGAGTGGAGGGCTGGGCAGTG CCCGAGGAGGGGAGGACAGTGGGACAAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGGCATGGGAATGACCAGGTCCACATCATGCACAGCAGGGGCCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTCTGCCCGCCCTA[C/A]CTGGAGATGCTCTAATA
TIGR- A005D24 b	138 C T ---	---	---	CATAGAAAGGAGCTTTGAGTATTGTACAGTTTGAAAATCTCTTTGAGATAATTGATTTCATATTC TGCGCTTTCAACCTCCATTACCTCTTGTCATCCAACTCTTTATAGAGAAATAAACCCCAATTT CT[C/T]TTCCACCATTTAGTTGATTATCATCTGGAATTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
TIGR- A005D24 a	123 A G ---	---	---	CATAGAAAGGAGCTTTGAGTATTGTACAGTTTGAAAATCTCTTTGAGATAATTGATTTCATATTC TGCGCTTTCAACCTCCATTACCTCTTGTCATCCAACTCTTTATAGAGAAATAG/AAACCCCAA TTCTCTTTCAACCATTTAGTTGATTATCATCTGGAATTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
U03735	74 C G ---	---	---	TGAGTCTGAGCAGGAGTTGCAGCCAGGGCCAGTGGAGGGGCTGGGCCAGTGCACCTTCCGGGGCC GCATCC[C/G]TTAGTTCCACTGCCTCCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTTCTGTTGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA GTTGTTCAAATGTTCTTTTAA
U39840b	42 T C ---	---	---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAAT[C]CAACAGCAAAACCAACACA CAAAACCAACCGTCAACAGCATAATAAAATCCAACAATTTTATTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCCAACCAATTTTTC
U39840	56 A C ---	---	---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAATCAACAGCAAAACAA[C]ACCAACA CAAAACCAACCGTCAACAGCATAATAAAATCCAACAATTTTATTTCACTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCCAACCAATTTTTC
WI-8997	41 G A CCCC	GGCCACTTGCT	TGTTGTACGC AGTGCTCA	GTGGCCATCGATCTGGACCGTCCCCTGCCCACTTGCTCCC[C/G]ATGAGCACTGGGTACAAACATCCA AAAGTTCAACACACAGCAACTGTGTCTCATGGT
WI-7008	180 A G ---	---	---	TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGTAGATGGGTCAGAA AGCACCAGTTTCATGATAGGCAGTTCAGGTCATATGGTACTTGTATGACCCAGAGTCAACATTCAG TTTCCACCAAGGCCAGTAACAGGCCAAGAGCTGCTCTCTCAAAAG[A/G]AGAGTAGTTATCTGCAGA AGATGGCAGGGGCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACT
WI-9005	26 C T	CGAATTTGCTG GGGAATCT	TCCCAAAAGTC TTAAGAAGAA AAA	GGTCCCACGAATTTGCTGGGGAATCT[C/T]GTTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGAGCGTCTCTCTGTTTTCTGGGTGG

WI-7593	46 G A ---	---	TTTGTGTTGCTCTGGACACCCACTGCTCCAGGATGAAGGAGAG[G/A]AATGAGATCAGTTTGGG CACTTCCTCTTGAAATATAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G ---	---	AGTGCATCTTGGGGAAAGGCTCCAGTGTATCTGGACAGTTCCTTCATTTTCAGGTGGGACTCTT GATCCAGAG[A/G]ACAAAGCTCCTCAGTGGTGTATATCCAAAGACAGAACCCCAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCATTCCAC CTATTCTGTGAAATATTCCCTGAGAGAACAGAGAGATTAGATAAGA
WI-7059	43 C G ---	GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAAATATACCTGGGTGAAATATACCAAATCTGCATCTCCAGAGGAAATTAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAAA
WI-9063	53 A C TT	TCTACTTTCTG CCTTGGGT	AGCAGCCATCACATGATCTGTTTTTCACCACCTCACTGAAGAGACACCATTTAT[A/C]TACCCAAAGGG CAGAAAGTAGAACTACTATTCTTAATGTTTGACACAATTGGAATTGTC
WI-7079	293 T G ---	---	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCACATACCATCTGTAGAGTTGGAACCTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTCTATTTCTTTTCCATTGCT TATCTTGAGCACAAAATGATAATCAATTATACATTTATACATCACTTTTGACITTTTCCAAAGCCC TTTTACAGCTCTTGGCATTTTCTCGCCTAGGCCTGTGAGTAACTGGAT
WI-9074	38 A G AAAAG	GACAGATTTT GACCTAGTTC TT	TGGATGCCGAGGTAAAAGTTCTTTTGTCTAAAAAGAA[A/G]AAGGAACCTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAAGGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T ---	---	GGAGTTTGCCCTTCTAAGGGAAGGAGATCTTATCTTCTGTTGGTTGACCACTGACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCCGGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCACGCAAGAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCCCTTGACCAAGGTGGGGGCCACAGCACCAAGCAGCATCTTG[C/T]
WI-7104	157 C A ---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTATCTTCTGTTGGTTGACCACTGACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCCGGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAAGGGCTTGGTCTGAGGAAGCAGATGTTTCAT GCTGTGAGGCCCTTGACCAAGGTGGGGGCCACAGCACCAAGCAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCAITTTAGTTGCCTAAGCATTGCCTGG[C/T]TTC CTGTCTAGTCTCTCTGTAAGCCCAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCCAGTCATCTTCTGTTTCCAGAGAGGTGGGGCTGGAT GTCTCCATCTCTGTCACACTTTAT[C/G]GTGCACTGAGCTGCAACTTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTCTCTCCCCAGTCATCTTTCTC/TJTGTTCCAGAGAGGTGGGGCTG GATGTCCTCATCTCTGTCTCAACTTTATGTGCACTGAGTGCACCTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTTTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGCGTGTCT CAGTCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTCTACGGGTCCCC TCITTTTGGCCCCAGTATTTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/AJACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTTTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/CJCCCTGGGT GCTCAGTGCCCTTTAAGTGATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTCTACGGGTCT CCCTCTTTTGGCCCCAGTATTTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAA CACACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGACCCCTTGGCTTCCCTC/TJGGCTCCAGGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCAGCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAGGCCGTGGGCCAAT GGGAGAGCTCTTGTTATTATAATATTGTTGCCGCTGTGTGTGTGTGTTA
WI-9171	62 G A ---	CTAGGACCCC ATTCTCCTATT	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAAATAAAGAAAGTAGAGATAATAATCA/G/A/
WI-9174	47 T C T	ACTG	---	TTCTTTACACCCGATGTAATTAAAGCTTGTATTACAAAGACTTCATGC
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA	---	GTGTGAGACCATCATGGTGGCAGCTAGGACCCCATCTCCTATTAT/CJAGTCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-9186	76 G A CCGA	CCACTTCTCCG CGCA	---	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAAGAACAGAT/A/G/ATCCCTGTATT TCAAGACCTCTGTGCACCTATTATTAACCTGCCCTGCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9193	94 G A CA	AGAAATTGT CTGCCCTTAAAG	---	AAAGAACTACAGAGGACGATGTCCAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA/G/AJACCTAGGTGAGACTTTCCCTTTTCATCTT
WI-9015	48 C T ---	---	---	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGTCTGCCCTTAAAGCA/G/AJATCCCCCTTACCACACACACACCCCTGTCTCTC
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	---	TTTGGATTGATATCGTGAATCCTCAGCCGAGAAATTTGGGTGGATTG/CJGCTTTGGTTAATACAT CTTTCCCTAAAGAAAGATAAACACAAAAATCCATCCAGGTAGCTCGGCACCACCACTAAGAA GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGCCAC/A/GJGTCCCTAATGACACCCACTCCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGAGGAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 GC	CAGTCCCCA GATTGA	CAC TTGCCAC ACTCAGAC	GTGACCCCTGTGAGGTCAGGTCGCCAGATTGA/C/GTCTGAGTGTGGCAAGTGTGTCAAAAGGGG TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTTGAGGCCGAAGATCA
WI-7836	120 T C C	CAAAATAACA ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGAAATAGAGAGTTGAGATAACACTCTCAITTCAGTAGTTACTGAAAGAAACTCTGCTA GAATGATAAATGTGATGGTCTATAACTCCAATAAACAATGCAACGTTCC/T/C/GATTTCATAAT CTTGGTTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACACAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAACTGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTTGGCCCTGCAGCATGTCTGCCAGAAITTCAGCTTCAGCTTAACTGACAGAT/C JGTTAAAGCTTTCTGGTTAGATTGTTTCACTTGGTGATCATGTCTTTTCCATGTGTACCTGTATAATT TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTT T	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAACTCTGGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAAT/T/GTATAGATGTAAACITTTAATAAAATTTGGGTGTGG GAAGATTAAAGGAGGTTGCTCTGTGCTCTCTCCCTGCCCTCCCCA/C/A/GTGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCTGGACCACTACTGGCTTATGGTTGGGGTGGTAGGCAGG TGAGCGTAAGTGGGAGGAAATGGGTAAAGTCTACTCCAACCTAGGTCTCTATGTCTAGACACCAG ACCTAGGTGCTTCTTAGGAGGAAACAGGGAGACCTGGGGTCTGTGGAT
WI-7860	50 C G ---	CGTACCTCCAA ACATAATTGA TTC	GCTTGAGTGA AGTCTGCAGA	CAAGGCGTACCTCCAAACATAATTGATTC/GTATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGAGGCGCTGGCTACTGTCTCTCTGCACTCTGCTGCTTG CACACTTGCTGTTCTTCAAGTCTGGAGTCTCTGGAGGTCAGGCTGGGGTAAGCCGGGTTCCACA GGCCCCAGCCCTGGCAGGGTCTGGCCCCCAGGTAGGGGAGAGCAGTCCCTCCCTCAG/GTAACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACTCCTGAAGCCAGCTTGCACTCCAGT TTGCACAGGGATTGTCTGGGGGCTGAGGGCCCTGTCCACACCCCGCC
WI-7307	128 G T ---	GAAATGTGAC TTCACTTGGT G	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTTGGTG/C/TJCAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTTGAGGTTGAAA AATTCCTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGCTGTGATTAACTCTTAAAT TGTTTGCAGTCTTTTATGTTATCATAGGTATAGGTGACCTAAITTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTGTATGTTTAAAGTAACTTATATCTCTGGATTTCATG AAGGTGAATAATCGTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313e	266 T C ---		---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGCTGTGATTAACTCTTAAAT TGTTTGCAGTCTTTTATGTTTATCATAGGTATAGGTAGGACCTAAITTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTGTATGTTTAAAGTAACTTATATCTCTGGATTTCATG AAGGTGAATAATCGTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256 C T ---		---	AAGGTGAATAATCGTTTGTAACTGAATAGAAATGTATAGCGATGA

WI-9281	68	G A	---	GCTAACACCTTT TTAAACCGT	---	CATTATTTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTGAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G]A[GTGTTAGTTTGCAGTCTGTGTGCTTCCCTCTCTTATGACTGTGTCCTC
WI-7848	142	A G	CTC	GTATATTACA ATGATCACCG ACTGA	---	CCCCACAGAAC TATTGTAAAC AA	TTCTGAAAATATAACCCAGCCATTGAGCTATTAAAACCTTGTAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAAATAAACATTAAATGCTAACACTTTTAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAATAAATGTAAATGGT
WI-9304	70	G A	ACTGA	---	---	---	TCACGTTTGGTGCTTCAGATTTCTGAGGAAATGCTTTGTATTGTATTAATCAATGATCACCAGCT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGGCTGTTTTTTGT
WI-7933b	314	C A	---	---	---	---	TTACAGAAACTTGCCTGTGCCTGTGTCCTCCCATGCTAGGGGCGAGGGGTCTTTCTCTCTTTCT TACCTACCCCTTTCTCTTGGCCAGGGCCTCGTATCTACCTTCTCTTGTCCCTGGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCCTTGGGGAGGAACCATAGTCCCT
WI-7933	96	G C	---	---	---	---	TTACAGAAACTTGCCTGTGCCTGTGTCCTCCCATGCTAGGGGCGAGGGGTCTTTCTCTCTTTCT TACCTACCCCTTTCTCTTGGCCAGGGG[C/G]CCTCGTATCTACCTTCTCTTGTCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCCTTGGGGAGGAACCATAGCT
WI-7374	182	T A	---	---	---	---	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAAATGAAAGAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTGTTGAAGAATATATTGTT[A/C]AGAAACACACAAGGCTT GAT
WI-9343	78	C T	CCTCTGCCA	CCAACAACAT CCTCTGCCA	---	AAATGAAACTTT ACGTTTTGTG TG	GGTCTGCTCTGCTACCTTGACCCCTTCCCTTCCCTCTGCTCTCTCTCATCATCTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAACAACGTAAAGTTTCAATTTGGGCAAA
WI-7386b	104	T A	---	---	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A G	---	---	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAAAGTTCACCTTTTGTATTAT GCTCTT[A/G]TGATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79	T C	TTGG	CTTTAGAAAA TCTGCTTTAAC TTGG	---	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAACTGTG CTTTAACTTGGT[C/AT]CCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T C	GTTC	TCCTGGGCTGT	---	GGTCCAGAAGA GCGG	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGACCCCTTTTGAAGAGGTGGGTGAAGTCTCCTT GGCAGGGATTGTGACACTGCAATTCCTGGGCTGTGTTCC[T/C]GGGGCTCTTCTGGACCTTGACCCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCCTGGAGGGTGGTGAATAAAGGCATCTACTGTCT

WI-7424	131	T A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGGAGAGCAGAAGTTAGAGAAAAAAGCCAGCGAGGAAAGG AAAAAACATCGCCAAACCTAGAAACGTTTTCATTCGTCATTCCAAAGAGAGAGAGGAAAGAAAAA TTA)ACAACTTTCATCTTCTTTCACGCTTCATAAACATCTACATA
X86400	118	A C	---	---	TCCTGCAAGAAGTCTCAAGCCTTTTGATTTTGTGCAATAAGTAGACAGCTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTTAATTTAAGTGAGA/CJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAAATCTAAAATATGTACCACCTGTTTATTTGTTTCATTTCATCCA TCCCTTTCCCATGAATATTCA
WI-8053	242	T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTCCACAGCAGCTCTATGATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAAAAGTGTCCTCATTAAGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAAGGGTCACA ATTAATCTTTGAICITTTTACTCACTGTTAACTTATATAATTA)TTTCAGAAC
WI-6190	165	G A	---	---	TACAAATGAATTCGTTTTATTTGGGTATGCATCCACATTTTCAGCATTTAGTGGTCTGAAACAGCAAG TGAAAGACGACGCAATTTGCCAGGAGGTCAAGCCCAATTTTCGGGATCTGCTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG)A)GAAGCAGCAGCAGCACCACCAACCAAGGCATGCA COGGATTCAAGGTCTTTTGTCCAGTTGTAGATCCAACTAGACCCCA
WI-6275	148	G C	---	---	AACAGTCAACCAACCAACCATGACAACCTGCCAGGCAAGGCTTGTCTCCCTCCCTCTTTCGCTCCC ATGTCCTAGTCAGCAAGGTGCGGGAGGCAACGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA)G)G)GAAAGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCAGTAACTGGTATGCTGAA
WI-6421	41	G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGTTG)TGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACAAA GAATATTTGGGGCAGAACCCCTGGAACTGGCCACCCAGGACATCCCAAATATCCCTCTCTCAGGG CTCACCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T A	---	---	GGGTGAGACGGGTTTATTTGTGCACATTTACACAGCGTCAACAGCTGTGGGCTGGCAGCGGCCATGCTC CTGTGGTCGGGCTGCTACAGGGCGTTCACTTTCTTCCACACACTATGTACAGTCAAGTCTCCAA GGTGATGGGCTACAGTCTGCATCAGTGAGTCTGTACACACATTTTACATAAATTTACACAGACTC ATACATGAAAAATTA)AGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAA
WI-9420	202	G A	---	---	AACCTGTTTACAAAATAGGCTTTGCAAACTTCACTAGTAATGTAAGTCAATGACTGTGTTGTTTT TAAAAATATGTACCAAGGAAATACAAATTTGGATATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAAGGATACGTGCACAAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG G)A)GCATTTCTTCTACCTTAACTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184 G A ---	---	TGGGGTGCCTTTAGACTTCATTTCTAGAGCAGACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAATCTCTTTGGATGCCAGTCCAGATCCC TTTTTAAGAAAAATGGGCTTGTTCCAAAGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAAGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204 G A ---	---	ATGTCAGAAGAGACACAGACAGGAGTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGCAATATGATCTCCCTAAAGCCCCAGATTCTCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201 G T ---	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCCTGATGACATCTGCTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAAGTACATCCTTGCCCTCTCTGAGGG[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85 T C ---	---	GATGATTTCTGAAGTCCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGT[G/C]GCTGATGACATCTGCTGAGCCATGTGCTGGCATCACAGGGT GGTTTATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAAGTACATCCTTGCCCTCTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149 G A ---	---	TTCAAGTATAAGGACAGGTCTAGAACAGCGTTCCCAACCTGGCACCATGACAGTTGGACCAAA TAACTCTTTGTTTCAGGGGACTGCTCTACACATTGTGGGATGTTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCCAACAAATCATGACAAATGAAATGCTTTAGACATT GCCAAATATACCTTGTGGGACAAATGGCCCTGATTGAGAACCCACTGGTT
WI-5385	110 G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAATGGTGACTCCAAATGGTGGGATTGAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199 T G ---	---	ACCAACCGTTGGCAAAGGCTCCCCAAGACTCACCACCCCACTTTGGTGCTTACCCCTATGCCGGGTG GGATTGAAGAAATAACCATATAATTAATGCTACAAATTTTCCAGTAGTTACCAGGCACCAGCCTAT TGGAAGAAATCAATAATGTAACCTACAATGATTGCTCTCTGGCTTGGTGCCAGGCATAGAGTT/G JGGCTACAACCCATTTATCATTGAACCCCTCAGAAGCATCCAGTTGGGCT
WI-5801b	157 G A ---	---	TGGTATTTTCTTTCTTAAATGTTATGATTAAATAGTGCTTTGTAGAATTTGAAAAATGTAAA TCAGAGAACAGAAAAATAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]JAGGGAATGAGAAAAAGCACAAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTCCCTTTCCCTAAATGTTATGATTAAATTAGTGTCTTTGT[G/G]GAATTTGAAAAAATGT AAATCAGAGAAACAGAAAGAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGAATGAGAAAGACACAAACAGAAAAAAGTGTGT GGCTTAAGGAAGCCAAAGGAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTTAAATCCGTGTCCTCATTCGAAGACTGCATTAGTCTGATGAGCCTTAGTTTC[C/A]TAA AAGCCCTCAGACCCGAGGACAATGTTTCAAGACTAAATGACTGAGGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGAGATGACTTTATAATAGTGGCAAGAGACAATCAGGAGAGCTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTATTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCGTTGTATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAACGCTCCTCACTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGAGTGTGTCT[C/T]GTCCCTGTTGGTCCCGAACCCAGTGTGGTGCCTGGCACAGAG GAGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCAGCTGGGATCAAGGACTGATAAAGCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTGGTATACCTTCTCTTCTGAAGACCAACCCCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCTACATCTCGAAAGACTAGATGAGTTAGGCTCTCTCATCT CAATTGAAATCTAGAA[G/A]AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGCTTGTGAAGCCACACAGAAGTATCTACTCTCTTTAC[C/T]AAGTGTACTTTTGA TATATTTATGGGATGATCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTTCTCT TTGTCAGGAGTTCTTATTGGCCCTTCTTCTAAACCCCTAACCATTTCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAACCTCGTTGGCTCAAAGGAACTGTAG[C/A]AAATCTTTTTTTTATTTTGTCTTTTAACTC AAAGAGTGGAGTTTGACCTTGACCTTGATGGCAGCTGCTCTTTTGTGGTAAATCCTCTAGT GGGCACCTTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAGCAGACAAACACTCCAAAGATAC[A/G]AGATATAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGCGATGTCAGACCAAAAGACATTTGGGTCT TGAGGTTGAATAGGAGTTGTCTGGTGAGTCTGCCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GATCTTTGCGACATGCAGAGCAGATACGGCAAGGCATCTTTGGGCATTTGGAAGGAACAGGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAGGCTTGTC[A/C]TCTGTCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167	A G ---			TGGTGAGGAGCTGAAGGCTGAAGAATAGTCTCTGCTCTGGTCTTCGTGGAAATGGATGAGTCCT TTTACAAAATTTTCTCTTGCCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGT[G]TGAACCTGAGCAAGTGCTCTTAATGTCCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198	G A ---			GGGTTCATTTAACAGCCTTCCACTGGGTCTCAGATTGACGGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCTCCCACTCTA CCGCCAAAGCTACCTTTGGTCTTTTATTTCTGCTAATGACCATACTATTCCCAATTAGA[G/A] CCATGICATTTTCAGAAAAGCAGTATA
WI-4823	164	C A ---			TTTATCTTCCAAACCATGTGTGTTCTTCACATACCTTTACGTAATTTAAATCATGTCAITTAATTA TGCACTTACTTGTGGCTACCGACATTGCTTCCAATTGTAATTCCTTAACACAGCAAGCATAACT GATGTGCCATCTTTGTTATTCCTAAA[G/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACCTCTCTGTTATTTCCCTATTTCAGCATTCATGATTA
WI-4860	72	A G ---			AAAAAACAACTTCATTTGACATTTCTAAGAAGATAAGAAAAAACACGATCCACTGTGTGTTGCTT GATTTA/GGGAGATAAACCTGATCTCTAAGAAAAATTAACCCAAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTCAGGAAGAAGCCCAATCCAACTAAGTTGCTAAGAAAAATATGTTTCATATCA CTCTAACTTCCACATAGCATTAATATAGCA
WI-9705	111	C A ---			TGAAGGACCAGTTTCGAATGCCTACCAAGTAAAGTAAATCGGAGGGGCGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATCAGGTTCTTTAAGGAGTTCGGCTGCC[G/A]AAAATTTTAACTGATGC TGCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATATTGTTGCTGTGTTCTTGGTG
TGR- A004Z48	177	A G ---			CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTCAATGAAGGTGGGCGAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGAG/GTCTCCAAATTTCAAGGGGCTCCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34	T G ---			GGGATTCAATGTGTCTGTCTCATCCAATAAGCACT/GJCATGACCTCAGCCCCCATCTTTCTTCCC TATGTTCCAGAGACAGAAATAGACCTGGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTTCTAGTTGA
WI-7747b	88	T G ---			GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCTGTTAACTGTGTATGTACATA TATATATTTTAAATTTGAT/GJAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTTGTGTTGGGTATCCTGCCAGTGTTGTTGTAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTATAAAGTATAATTTTTTATGTTTGTCTGA

WI-7747a	44 T C ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGC[T/C]TTCTGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAAGAGCTTCAATGCTTTTGTAAAGTT ATTTCTGTTGTTTGGTATCCTGCCAGTGTGTTGTTAAATAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAGTATATAATTTTATGTTTGTCTGA
WI-7189	197 T C ---	---	TCCAGAAATTTCTCTTCAGCTCATTTTGCTCTCTCACAAATTAAGGAGTAGGTTAAGTAAAGGT CACATACCATTTATTTCCCTTCAAAACAAATAATTTTACAGAAAGCAGGAGCAAAATATAGGCCTTT CTTCTAAGAGATATAATGTTTCACTAAATGTGGTTATTTTATATTAAAGCCTACAACATTTT[T/C]AG TTTGCAAATAGAACTAATACTGGTGAAATTTACCTAAACCTTTGGTTATT
WI-7850	57 G A ---	---	AGCCCAGCTGGACTCATGGATGTCACCCCTTTGCTCCCTGCTCTTCTGCCCTGG[G/A]CTCATGTA TCTGCGCAGCTCTGGTACCTCTGTGGTGCCATCTACCTCTGACACAGACTGCCTGCCCTTGAAGCT GAGAAAGCACAGGGCAAGGAGCAAGGACCAAGAGCCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGCTACTAGAGCC
WI-7907	69 G C ---	---	CTCTCTCTCATCCCATCCCCCTAAATAGGTCAAGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTGTTATTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCCTAAATTTATATCTATAAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATATTGTCAAAGTTTAAAT
WI-7919	242 T C ---	---	GAAGGCAGCTGGATCACTTCCCGCAGTCTTGGGCAGCGCTTGTGGAACACAGAGCTCCTCCT CAGGGCCTGGCAGCTCACTTCTATCTGTATGATGATTTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTTAGATTTTCTACCCCTAATCTGTTTAAATTTGTAACCTTTATTCATTTGAAAGTGTCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT[T/C]ACAACCTT
WI-7928	101 T G ---	---	CTCCCTTCCATATGTCTCTCAGCAGCACGTTGGGGCACACTGTTTCATCTCTGACCGTTTCTGGGCTA TTCCCTCTGCAGTGCAGACATCGTCAAAATTCAT[T/G]ACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAAATAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131 T A ---	---	TTTTGAGTCAAAGACTTAAAGGGCCCAATGAATTTATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTTCTTTGGAGTTAAATGCACATATAGACACATACACCAACACTTACACCAAACT[A] ACTGAATGAAGAAGTATTTTGGTAACCCAGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C ---	---	TACACGTTCCAGCCGTTGCCCACTCATCTCGCGCTTGTCTTTGGTTGGGGGCAGATTGGGTGG AATGCTTTCCATCTCCAGGAGACTTTCATG[T/C]AGCCCAAAGTACAGCTGAGCACCCCTGGTGTG TGTAAGTGTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCCAATGGACAGTTACACTTGACAGA CAAAGATGTTGGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	TTTCTAGGCTGTACAGTCTGATGCAATGATTTTATAAATATTTTCACTCTTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGT[A/G]TTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTCAATTGTGGAATAGTTTAAACAGTCAGGAAGGCTAAACGGTCAGTATTAAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	GGCCAGGAGATTAGCAACAAGGATTCTGTTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGAACAGACACTCAGTGTCTTGGCAGTGT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACAACCTCAAAAAATTGGCAATGTCAATCAG
WI-140	252 C T ---	---	ATTTGAAGATTGGAGGGCTTTCAGAGGAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTTACCAAGTAAAGTTTATA TCTCCATTAGCCAGCTCATTTGCCAGAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAATTTAGTTTAAAAATGTGTCTATTGTCTGTATTGGCATTCCT[C/
WI-198	218 C T ---	---	GAGGCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTCCCGGATCAAGTGTGCTGGCACC CATGATGGAACCTCTTGCCATGTTTAGTACCCTGGAGCAAGTAGTCAATCCATCCTGACTTTTAAAA TTCTAAACAGCCTTTGATGGGACAACTCTGCTGTAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTCCCTTT[C/][G]TTTAAACAAAGCATAGAAATTTCTGAACAACT
WI-205c	146 T C ---	---	TTATGTTGCCAAGACAGATTTTAAAGAAAGAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/][C]CAAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	TTATGTTGCCAAGACAGATTTTAAAGAAAGAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/][C]CAAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	GAAGACTGAGTTCCAGGAGGTTCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNCCTTCCAGAGGCTCAGACTACCTCCTCCTCCTCCTCCT CTCCCCACACACACAAATACAGAGATT[G/C]AATTACAGGAGCCAGTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---	---	AGCTTTTGAATCCAAAAACACAT[A/G]CTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCCTGAACGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCCTTGCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ---	---	---	AGCTTTGAAATCCAAAACACATAG/CITTGACTCTCTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCTGTGGCTGCCTAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAATTTAGAACTACTTCC[G/A]GTTT TTCCCTGGGAAAATATTCAAAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCATTATTAGAGCCAGGGTCTTGCTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	---	CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	---	CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	---	CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATATGCCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATCTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---			TTCAAATTTAACACCATGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGTCTTGAGCTATTAACTGATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCTCACCCCTACTTGGGCTCTGACTTCCTTCTCTGGGCT GAACCTTCTCTGTGTGGCTGTCCGCTTCTCTGCTTGGGCTCCATAC
WI-681b	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACAGGGGAAGCACTTTGNCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATAGTATGGACCAATTTGGACACAGATTATATATGTCAGA CACCACGNATGCTCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACAGGGGAAGCACTTTGNCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATAGTATGGACCAATTTGGACACAGATTATATATGTCAGA CACCACGNATGCTCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGACATCTTCCCTTTTCATCTCCGJAJTTTGTGTTGGC CAAATAATATCTCCCCAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAATGTTATCTTATGC AGTGTATGGTTTGAATGTGTCCCCCACAAAGCACACATTAGAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGACATCTTCCCTTTTCATCTCCGJAJTTTGTGTTGGC CAAATAATATCTCCCCAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAATGTTATCTTATGC AGTGTATGGTTTGAATGTGTCCCCCACAAAGCACACATTAGAACTTA
WI-867	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGACATCTTCCCTTTTCATCTCCGJAJTTTGTGTTGGC CAAATAATATCTCCCCAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAATGTTATCTTATGC AGTGTATGGTTTGAATGTGTCCCCCACAAAGCACACATTAGAACTTA
WI-871b	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTCTGCATATGTAATAAGGAAATGATAAGAGACACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATGTGTACCC TAAATTCATATGTTGAAGCCCTTAACACCCCAATATGCTGTATTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTCTGCATATGTAATAAGGAAATGATAAGAGACACCCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATGTGTACCC TAAATTCATATGTTGAAGCCCTTAACACCCCAATATGCTGTATTGTACATAA

WI-884	198	T C ---	---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAATTCCTATTTTGGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGACAAACNNAAGGAATA[T/C]G ATCCGGCATGCAACATTTATTAGTGAAACACATGATGAAATGAACATAAT
WI-921b	205	G A ---	---	---	CACCTCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTTACTGG CAGTGATGCCTCTCACGCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTCTCCGAG
WI-921	205	G A ---	---	---	CACCTCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTTACTGG CAGTGATGCCTCTCACGCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGCAACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATCTCTCCGAG
WI-945c	90	G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNATGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90	G C ---	---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNATGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167	C T ---	---	---	TTGCTTCAAAGAAGTTCTTGTCTCAGGAAGTTATTCATTGACCAACCTAAATTTGTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTC/TCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A ---	---	---	TTGCTTCAAAGAAGTTCTTGTCTCAGGAAGTTATTCATTGACCAACCTAAATTTGTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C ---	---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTGCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTATTACTTTGGGAGAAATGCTCAACTATAAATAATTGCTTCTGACCCCTTTCTGTGTC CTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAAATNTG

WI-1147b	204 G A ---			TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCAGGGTTTTCACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGAACTTCTCTCTCCCTGCTGGCTC CTGAGCCAAAACAGGCATTACCATAAATCACTTTGTTAGGATGAACCTTATCTGGCCAAACTGATA CIG/ATGCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---			GCATTAGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATGCGCCAGGTGGC TAAGTGTGGGG[C/T]CTGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---			GCATTAGAGGGTTCGTTTAAATGACATTCAGTGGCCCTGCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---			AAGTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAAAACATATGCCCA TCATCTTCAANGTCCACAGACACITATCCCTTAGACAGCCATTCTTTTGAATG[N/C]GNCANT AAAAATGATTTGAAATTTGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 C T ---			TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTCCATT[C/T]TATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCACA TCCACTGCTTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305c	46 C T ---			TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTCCATT[C/T]TATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCCTC ACATCCACTGCTTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305b	153 T C ---			TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCCTCACA TCCACTGCTTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305	202 C T ---			TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCCTCACA TCCACTGCTTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTTCTGCATTGGAATAGTTGACCTTCTATGAGNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGTGACTGTGCTGGTCAITTTAGAAGCCATAGAGATGAAGTGAAGCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTA/GJGC
WI-1306	240	A G ---	---	TTTCTGCATTGGAATAGTTGACCTTCTATGAGNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGTGACTGTGCTGGTCAITTTAGAAGCCATAGAGATGAAGTGAAGCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GJCTTCCTAGC
WI-1307b	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGGAGCAGTGGTGAAGCAAT/CJGTGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNTCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGGAGCAGTGGTGAAGCAAT/CJGTGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNTCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTCTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTT/CJACCCAGCAACTTCCCTTGAAGGGCAGGC ATTATGATTCACACTTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C T ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTCTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTT/CJACCCAGCAACTTCCCTTGAAGGGCAGGC ATTATGATTCACACTTTACATCAGTGGGAAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T C ---	---	CTACGATAATTAGTTTGGCAGTGAAGGTATTAGCTGTGTAGTGAAGAGTCTGTTATTTGTAAA ACACCAAGTGCAGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT/CJGAAGTTGGGTAGCTACAGGCTCCCCCAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTCCATCTCTAAG
WI-1327	175	C G ---	---	CTACGATAATTAGTTTGGCAGTGAAGGTATTAGCTGTGTAGTGAAGAGTCTGTTATTTGTAAA ACACCAAGTGCAGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAG/CJTAACAGGCTCCCCCAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTCCATCTCTAAG

WI-1341b	136 G A ---	---	TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGNNGNNTCTTTTCTNNTT ACCTGATCCACTATCTCTCAAGATCANGTTCAATTTGGCTNCTTTGTTNAAATATACCCAAAGC [G/A]GGATTGTGATGATCTGTTATTTCTCTGTGCTTGGACACGACAGAGTCGTCTGNGAGTNTG GTTTCAGGATTTGCTCTGTTTCCCGAGCCCACTTGCACCTTAGCAAGTGT
WI-1349e	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349c	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATATGAT
WI-1403b	57 C T ---	---	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTGC/TJTTCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATCTTGGCCTGCATCATGCATTTGGCAATATGTCACATAGCTGTCCCTCA TAATCCCCAAAGTGCCAAAAGGGTGTATCIGATTGT
WI-1403	58 T C ---	---	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTGC/TJTTCCGAAT TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATCTTGGCCTGCATCATGCATTTGGCAATATGTCACATAGCTGTCCCTC ATAATCCCCAAAGTGCCAAAAGGGTGTATCIGATTGT

WI-1417c	31 C T ---				CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTTGAGGGCCCCAGAGGAATCCCAGTGGCCCTCTCAATGACATTG GGTCTCTGACATTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGGTCGGTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTTGGTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---				CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGGGGAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTTGAGGGCCCCAGAGGAATCCCAGTGGCCCTCTCAATGACATTG GGTCTCTGACATTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGGTCGGTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTAAATGTTTGGTTGTAGAAAAAGTCGC
WI-1729	172 A ---				CCATGAGCAACAGCATGTTTCTACTCTGTGATGTGATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTTACAGGCAATGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGCTCTCCGTTGGTACCTTCTCTCCACCACATCAGCTGTGTTTTT
WI-1732b	122 T C ---				TGCCTTACTCTTTGTTCAATCCACCATACATTTGTAAATTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTT/CJATTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGTGGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATAATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1732	114 C T ---				TGCCTTACTCTTTGTTCAATCCACCATACATTTGTAAATTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCCCTTATTTCAGTCT CTGCCACATGCTAGTAACTGTGAGTGATGGTGGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATAATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1750	97 A G ---				GCGAATTTAATGACTCCAAAGGTAGTAATCCTTTCCTCCCAAAAAAGGTTTAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGAG/JTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCCGGCTTGCAGTCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---				GGTACACAAAAGAAATGCTTCTGGAAATCTAC/JGTAGGGCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAAGTACAATTAC TGGGAAACTGTAGAACAAATAATTCATAGTTTACACATAGCTGGGAATCACTCATGTGCCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAGAAATAATCATAAAAAT
WI-1803c	77 A G ---				CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT/JGAGTAGGTAGAGCATCACACTTGGGAGGACATAATTCGGAGTNAGATATCCTG GGTGCTAAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTACTCTTGCTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G ---	---	CCACTCAGTAATAAGTTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATAGTAGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTAGATATCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAAATTACTTACTCTTGTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAAATACTGGAATCA
WI-1837b	112 C T ---	---	TTTACTGGGATTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC[C]/TCTGTCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAAACAACCTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1837	112 C T ---	---	TTTACTGGGATTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATAC[C]/TCTGTCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAAACAACCTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGCTGTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G]/TGAGAACTCTGAATATTCAGGACATACAAGTGACAAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTCTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G]/TGAGAACTCTGAATATTCAGGACATACAAGTGACAAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTCTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCACGTGATGCTGTTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTT[C]/TGTGTCNAAATAAACTCCCAAAA AAGTGTTAGTCCACAGGGTTTAAAGTCTTGTGAATGAATTTCTGTGCGGACCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCACGTGATGCTGTTTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTT[C]/TGTGTCNAAATAAACTCCCAAAA AAGTGTTAGTCCACAGGGTTTAAAGTCTTGTGAATGAATTTCTGTGCGGACCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTGTGTCAGGCAACGGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTACAGCTGCAAAAGAGG[C]/TGCTCTGAGAGGT AAAGTGCCCTGCCCCAACGGGCACAACTAGAGAGCAGCCAAACAGGTTTGAACCCAGCTGTGCT GACTCAGATCTGTGTGCTTAAGTCCCATGAGAAACCACTTTTCTTGTCTCC

WI-1900	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAACCCCNNG CTNAGGTAGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG[C/][T]GCTCTGAGAGGT AAAGTGCCCTGCCCAACCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAAGTCCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165 C T ---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAAGCC[C/][T]CTCTGAANCCTGGTCCCACGTGGAGATAGTAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T ---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAAGCC[C/][T]CTCTGAANCCTGGTCCCACGTGGAGATAGTAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T ---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTGGAGTAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCATGCANGTCTGCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960c	270 A T ---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTGGAGTAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCATGCANGTCTGCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 A T ---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTTGTCTTAGTCTGTAATAACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCCTTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C/TAACAAATCAACACTGGCTGAGGCTGTTGG
WI-1977	203 T C ---	---	AAATCTAGAGCCAGAAAGTCAGCTCAGGATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAACTAGCTAAAAATC[C/][T]TTAAATCAGTTACAGAGGCAATACCT GGGTTAATGTAGGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACCTTTTTTCTACTCTCATT GGCTTACCAATGCTTCCACTGGATC
WI-2012	102 T C ---	---	

WI-2013	127	C T ---				CTTTAGAGGTGGTCATTTCCGTTCCCTTCTGGAAAGTGATTCGTGTTTAAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATTAATGCTGATGACTGACACTTC/TCTCA CCAGAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGGATATCTCAGCTTTCGAGCCCTGTTACTGCAATCC
WI-2032c	166	G A ---				ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTCTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCCACTGTTTCTAGATGTACACG/GATGTGGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACCTTCCGTGTAATGCTTCTGTTTTCAAAGGG
WI-2032b	219	C G ---				ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTCTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCCACTGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTCCTGTAATGCTTCTGTTTTCAAAGGG
WI-2032	219	C G ---				ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTCTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCCACTGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTCCTGTAATGCTTCTGTTTTCAAAGGG
WI-2054b	188	C T ---				CGTTTCTCTACATCTGGGNNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTGGA TTTTATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/TCTGCTGCCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGAATGGGCTGCTTT
WI-2054	183	T C ---				CGTTTCTCTACATCTGGGNNACATAAAGANGAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTGGA TTTTATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/TCTGCTGCCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGAATGGGCTGCTTT
WI-2573d	129	T C ---				TGGGATTAACACCCCTGTTTCTCTCCAGTTTCAGTGTGCCTTAATGTTGTGCTAGAAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTTCAAGGTTTCCGTGCTT/C/TGA TATCATCTGATCTTCCCAACAGGCTTATTTATGCCTAGGTAAGGGTTAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C ---				TGGGATTAACACCCCTGTTTCTCTCCAGTTTCAGTGTGCCTTAATGTTGTGCTAGAAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTTCAAGGTTTCCGTGCTT/C/TGA CATCTGATCTTCCCAACAGGCTTATTTA/C/JTGCCTAGGTAAGGGTTAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG

WI-2573d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTTCAAGGGTGTTCGGTGTCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTTCAAGGGTGTTCGGTGTCTT[GATAT CATCTGATCTTCCCAACAGGGCTTATTT[C]TGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTTCAAGGGTGTTCGGTGTCTT[GATAT CATCTGATCTTCCCAACAGGGCTTATTT[C]TGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573a	129 T C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTTCAAGGGTGTTCGGTGTCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2868b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTCTTAATTTACAGACATTAAAGAAACAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTCTTAATTTACAGACATTAAAGAAACAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCCTCTGCAT ATCATGGAAGCCCAACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 T C ---	---	CATGCTGTGTAAACCTCTGTGCTGCTTGGCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGAT[C] AGAAATGAATAGAGCCCCATTTAAATTTATATACAGCTTTATGTCCACTTCCCTGCTGCCATCAG TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131 T C ---	---	CATGCTGTGTAAACCTCTGTGCTGCTTGGCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGAT[C] AGAAATGAATAGAGCCCCATTTAAATTTATATACAGCTTTATGTCCACTTCCCTGCTGCCATCAG TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	TTAGCACATATCTGTTGTGGGACTTAACCTGAGACAAGGCATATAAAATTAACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACATATCTGTTGTGGGACTTAACCTGAGACAAGGCATATAAAATTCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACATATCTGTTGTGGGACTTAACCTGAGACAAGGCATATAAAATTCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTCACCAGCATTTCTAAGAATTCG CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTTAAATAAACCTAAG ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTCACCAGCATTTCTAAGAATTCG CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTTAAATAAACCTAAG ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTAA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTAA AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTTTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTAA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT

WI-2995c	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGCTGGANTTTTTTNA AATCTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	C T ---	---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCTGTGAGATCAGACTGGAGCCAGTCCAGCTTGAGACCAC ATCTCAGTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCTCTACTCCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
WI-3234b	68	T C ---	---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATTCITTTATGAGGTCCATGTCCTACTCTTAT T/CJGACAAAGCAAGAACAAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTAAACAAAGTACTGTAGAGTATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGACAAATGGAATGTACTTATTTNATATCTTAT
WI-3234	68	T C ---	---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATTCITTTATGAGGTCCATGTCCTACTCTTAT T/CJGACAAAGCAAGAACAAACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTAAACAAAGTACTGTAGAGTATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGACAAATGGAATGTACTTATTTNATATCTTAT

WI-3292b	106	G A	---			GTTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTG[GA]TGGTATTTGGATGGGATGATTA GCCATGAATATTTTCCATTGTTTCTCATTAAATGATTAATTAATTAAGTAAATATTTATTNCCATGA GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCTTTCAATC
WI-3292	106	G A	---			GTTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTG[GA]TGGTATTTGGATGGGATGATTA GCCATGAATATTTTCCATTGTTTCTCATTAAATGATTAATTAATTAAGTAAATATTTATTNCCATGA GACACAATGGAAAAATGGAAACATTCATGGAAAAAACCCTTTCAATC
WI-3355	19	G C	---			CCATGAACCATGGGCTACA[G/C]ATATTCCTAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATATACTTCCCAAGCACTTAAACATCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTNNAGTTG
WI-3408	194	G A	---			CCATGAAGAATGAGTTCCCTCCCTCCCTGGGTACGTCCTAAGAATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTCTCCCGCTCTAAGACACACCTTTATGCTTTTNAAGCTTT CTGGAATGGGATGAATCTNACATTCATGTCACCCCTCGTGTGGGATCACTTC[G/A]TGCCCC ATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A	---			TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCATTTGTCACTAGTGCACCTTAAAAATATTTT GAAAAATGGCAATTTTAAATATCTTTGGAACCTCCTAACACATTACCTATTTTNAACCAAAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3505	131	G A	---			TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCATTTGTCACTAGTGCACCTTAAAAATATTTT GAAAAATGGCAATTTTAAATATCTTTGGAACCTCCTAACACATTACCTATTTTNAACCAAAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3564b	177	C T	---			GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGTGTACAGAGGGCTTGAGCGTGTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTCTC[TA]ACAAGTGTGTTGTTGTTGTCATC AGTGTCACACATGCTACCTTCCCTTCACAAAAACAAA
WI-3564	177	C T	---			GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGTGTACAGAGGGCTTGAGCGTGTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTCTC[TA]ACAAGTGTGTTGTTGTTGTCATC AGTGTCACACATGCTACCTTCCCTTCACAAAAACAAA

WI-4230	93 T ---	---	AGAGACGTTGAATGGGACATCTTTCTATTTCGATTTAGTTTAAACATTTGATAAGAAATGATGAAA GTTTGTACATTCAGATTTATCTTTATAGCAGCAGAGTCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGATGAATAGTGACCTTTTGAATTTTGAATTTATGG
WI-4241	118 CT ---	---	GAAATCCATTGAAGTTTGACCTTGAACCTGATCTCAATTAATCTTTTNCCTTGTAGTGGTTGTAATTT CATTTTGAACAACAGACAGAGAAAATTTCCACTTAAATTAATCTCTC/TAAAGTATCTATGAT TTAGCACTGTTAGCACCAGAACTGTGAAATTAATCTCCTAGATATCTTCAGAACTCTAGGATGGAAAG AA
WI-4271b	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---	---	AATCGAAACATTTGATTTTGTAAAGGAACACATTTATTTATGATATTTTGCCCGAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAGGATATTTGCATAACCTTTTGA AGGTAAGATGTGAACCTTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 G A ---	---	AATCGAAACATTTGATTTTGTAAAGGAACACATTTATTTATGATATTTTGCCCGAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAGGATATTTGCATAACCTTTTGA AGGTAAGATGTGAACCTTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G ---	---	GATGACAAATTTATGTTGGCATTTTAA[A/G]GTACCAATCCATTTTCTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGTTAGTCGATTGCTCCTTTTCTAGTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTTAATACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---	---	ACCATCAATGATCACCTTCTAAAAATTTATGATGATTAACCTGGCTCTGTTAAAAATAAAACCT GTCTTGGACATGAAATATAACATTAATTTGGTCATTTTCTGCTACTTACAAAGGTACTGCACCTA AACAAAGTTAAG[G/C]GTTTGTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA TTTCTTGCCCATAAATAAAATTTTACATGCCT

WI-4584	144 A G ---	---	---	TTGGTTGGCATTAGCCTCATAACAACATATTTACAATCAATAATGTTACTCTATTTTACAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGCAGAGCCAAAGATTTGAACCCAGGAATCCATT CACCGGTACAGJTGCTACCTGGTAAAAAATGTTTAATTAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAATAGGTGCTTTAATTTGTTATCAGTATGC
WI-4639	185 C T ---	---	---	TTTCTGCATTGAATGTGTATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACCTTCCAAATCCACCATTAC TGACCATATGACTTGGGGAACATATCTCACCTATCTGAGCTGTATCCGCTGATCTCTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAATGAAATAA
WI-5327	63 A ---	---	---	AAATGAATCCGCTTAGAGCAAAATACCAGTAAGGGCTGGTGAGGATGGTGGCTGAGAGA/A/- JGATTTACTATAAAGCATATTAAATTTATAAATATGGAATAATTAAC TAGATAAATTAATGTGAAT TGAGTTTGAAGGTTCATGAGAGTAGGAGGAGGTAGTTCTACTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTCGGATGACATGATGAAGTGTCTAAGCAGACAG
WI-5390	87 C T ---	---	---	GCTTTTGAGAAATGAAAGGGAGCCCTGGACCATTGCAGGGCTCTTCATCTGATTTTGTGTAT TTATTGTTCACTATTATTC/TGCTGTCTCCCTTCTGGTATGCTTGTCATGAACAATGAATTC CCCAGTGCCTGGCCGATTGCTGGCTCCTAGAGGTGTCAGAAAAAAGTTCCGGTGAATAGAATTG ACGAATGGGTTCAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A ---	---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAAAACATTATTTAATTTG/AJAAAGAACTTGTTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCAACAA
WI-5404	87 G A ---	---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAAAACATTATTTAATTTG/AJAAAGAACTTGTTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCAACAA
WI-5545b	77 A C ---	---	---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCCTC/AJCCCAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAAATGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
WI-5545	77 A C ---	---	---	TAGGAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCCTC/AJCCCAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAAATGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

WI-5860b	134	A G ---	---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGTAAAGATTTTATTGT TTCTTTTATATAAAATATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATGTGAAGACATTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGTAAAGATTTTATTGT TTCTTTTATATAAAATATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/ G]TTATACTGGAATCATGTGAAGACATTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	---	GCAACAACTTATTACCTGATTCACCCAGGTCTACTAACATTATCAACCCTAACCACAATAC TATATATTGCTCTGTTCTGAATTTTTCATTTAGAACTCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATCTTACAGAG TAATT[C/G]ATAGTAGGTCAACCAAGTCTATATTGTATGGAAGGAAAG
WI-6109d	129	T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCT[C/ AAACCCATATTNCTGCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147	T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTAA ACCTATATTNCTG[C/T]CTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147	T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTAA ACCTATATTNCTG[C/T]CTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129	T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCT[C/ AAACCCATATTNCTGCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6112	96	T C ---	---	---	AATGCCATACACCTTCCATCATGCTGCATAACTGATTGATTTCATAATGCTTATTGTCACCTGTC TTCCAACACATGCTGTTTGTTCATGA[C/G]GCATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTTGTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103 T C ---			TAATTGCACAACATTACATATCAGGGTTTCGATTGAAAGGAAGAGAATATTCTCTTTCTTTAGTGATT GCTTAATATTAATTCAATAAGTGCACCATCTCTTC/GCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACCAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124 C T ---			CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCAACTTAAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTC/GTACTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAAGAGTCG GGTTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234 C T ---			AGGTGCCATTAAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCC/GTJTGAGGACACTGACAGT
WI-6336	234 C T ---			AGGTGCCATTAAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCC/GTJTGAGGACACTGACAGT
WI-6381	92 C A ---			TTGGATACAAAAATTCAGTTACACAATCAGTAGCATCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTAAACA/C/A/GTATTTAAAGCTCAAACTTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCTTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGCAAAAGATCAGAGTTCAG
WI-6436	198 C G ---			GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCAATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAAGTTTAGACTTTGGTGGTTGTAGTGTAGTAGGAGTAGGAGCTT/C GIATTGGGTGTAATCCACAGACAAGGTGATGTTCTAAGATTGATATTTATTGT
WI-6449	186 C T ---			GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATGGTGGTGTCTCAGACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTATCATCTGCATCTCTGATCTTATGCTGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTCTGIGGGTATTATA
WI-6449	186 C T ---			GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATGGTGGTGTCTCAGACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTATCATCTGCATCTCTGATCTTATGCTGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTCTGIGGGTATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAGACCTCCAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGAAATTGAAA AGAACAT/CTGTGAAAAAAATTAAGTAGAACTCAAGAGAGCCAAAGTCCCAATTTGTGTCCATT TAAGAAATATTTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCTCTCCTC CAGTCCCATTTATATGACATTCGGATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACITTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACITTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAATCAATTAACITTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCCCAATAGTGGAGAATCAGAGT/AJGCTCCTTGTCAAGTGTGCTACAGA GAAGATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAATCAATTAACITTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCCCAATAGTGGAGAATCAGAGT/AJGCTCCTTGTCAAGTGTGCTACAGA GAAGATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCCCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA/G/AJTCAAATTTTAAAGAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTGTGCAAACTTATCAGTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC/G/AJCACTGGCTTTG TAGGCATTACATCATATGTCTGTCTCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTTGGGTCTGTGTAAAG GTTCTTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC/G/AJCACTGGCTTTG TAGGCATTACATCATATGTCTGTCTCTGAAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTTGGGTCTGTGTAAAG GTTCTTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA

WI-6608b	46 C ---			CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6608	46 C ---			CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6666	68 C A ---			GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTACTCTGTGTTTCATGTAA ATGTTGGGGTGACTCATTCCGCCTCTTCTTCTCAAGTCCAGGCTTCTTGGGTAGACCAAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G ---			AGATTAAACATAATTACTGGGGCCATTGTAGGGTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCCTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGGCCGAGTCAGGGTTGTGGGCCAGAGTTTAGACAAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTCTAGAAGGGAT
WI-6670	120 A G ---			AGATTAAACATAATTACTGGGGCCATTGTAGGGTNGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCCTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTGAGGGCCGAGTCAGGGTTGTGGGCCAGAGTTTAGACAAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTCTAGAAGGGAT
WI-6704c	33 T C ---			TTTGAAAAATAATTCATGCACCAATGTTTTAACT[C]ACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C ---			TTTGAAAAATAATTCATGCACCAATGTTTTAACT[C]ACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---			TTTGAAAAATAATTCATGCACCAATGTTTT[C]TAACTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNC GTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---			CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCCTTAAACACATTTTGTGAGGCTGGAATGATTCCTCC[G]A/TAGTAAACCTCAACATCCACACCT GCATAAACATCGCTCCCAAGTGACTATTATTACTGAGTCGACACAGGATGTCACCAAGTGAGCCTC ATCTCCAGTCCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---			AAAAAAATGGTGCAATGCATAATATTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6766	148 G C ---			AAAAAAATGGTGCAATGCATAATATTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6787b	97 A G ---			ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAATTTTAC[G]TTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGCTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---			GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAATCAATCAGTCAACCCCTC[G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37 T C ---			CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAAGCATTTTAAATTTTACAACACA AAGCTCAAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---			CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAAGCATTTTAAATTTTACAACACA AAGCTCAAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---			GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C]A/TGTGGATACCCGTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGITTCATAATCTTGTTTCAGGTGCGGCTGTGCAG

WI-6817	145	C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACTCATCACTAACTCAACAATGTAGCT GCAGGTAA[C]A/TGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGGGCTGTGCAG
WI-6819b	221	C ---	---	GATGAAAGCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAAATGGAAAAACATTTAGTAC CATATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAAATTTTCTGCTATTTTG CTTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGAAAGCCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAAATGGAAAAACATTTAGTAC CATATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G]CATATACAAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAATTTATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAATTTATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6826	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAATTTATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAATTTATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTTGAACAAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATAATTCACCTAAGTAAATACAGCAGATGAGATGTCCTCACATGTAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTTCAGTGTAAITTCACAAATATATAGCAGCTCA AACAAAAATGCAGGAGCAATGGCAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153	G A ---	---	TTATAGAATCTTATGGGGCATACNGTAAATGAAGTCAACCTTAAATCTAAACAACAGCTTG TTTGTTGTTGCTGCTGAAATCCTCCCTGCTCACAACAGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTTGAGGCAAACTTC[G/A]TAGAGCCATTTCTGTGCAGAGAAGGGAAGGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGCTGTTAGAACTGAGCTCAITAA
WI-6909	73	C T ---	---	ATTGAAAACTGGTTAGCAACAGATAAATACAAATAGAGCCTGGATATAAAAAATGAGAGAAGATGC AGACTT[A/C]AAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTGTAAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTTATTCGAATAATAAATCTGCCAGTGCCAAATCAG AAACACCATTTCCACAATAATTTGCATGCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163 G T ---	---	---	CACTCAAAACCTTTATTCAATTGATTTACAAACGTGTACAATATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTTCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	---	GCTGTTTTTTTTGTTTTTTTTAAGTGACACCTTGGCCTGTGGCAATTTCTTCACTTATCTTACCC AAAAGTCCCTTTGGCCCCAGCCACTGACTGATTTAAACCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTAATTCAGGTGATTTTCTATTTGGTAGTATTTTCAGATTTCCACAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C ---	---	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATGAAAGTTCACTCTTAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGT[C/A]ACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATGAAAGTTCACTCTTAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGT[C/A]ACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A ---	---	---	TTTTATGAACATTTCCAGATCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC[G/A]NGTCATGTCCCAAATTTCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATATTAAACAAAAATGNGTTTTTNGCAATTTATGTGAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	---	TTTTATGAACATTTCCAGATCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC[G/A]NGTCATGTCCCAAATTTCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATATTAAACAAAAATGNGTTTTTNGCAATTTATGTGAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---	---	---	AACTAAAAACCCCTTATTGCTCCAAAGTGTGGCAAAAATAGAAAA[T/C/G]TTTCAATTACATTAGG AAATCGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCAGTCAAAATAATCACAATA ACAAATTCAGATTGCTTGGATCTTGGTCAATTTATGGCTTGAAGAAGTGGATTTGAAAAACCACTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAAATCATGC
WI-6996c	242 G T ---	---	---	ACTTCTAGTGCCTCTGTTACCACCCTCTAATGCCTCTGGTCCCGCACTTCTGATGTCCTAGGCGCT TAAATCTGCCTGGCTGCCCTCCCTCTGTCTTCAGCAACAGAGGAGGAGAGCGCGCAGTTCCTCG CAGGAGAGAGGAGGGGTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTTCC[G/T]GTCGGATC

WI-6996b	242	G T	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGTCTTTCAGCACCCAGAGGAGGAGAGCCGGCAGTTCCCTGT CAGGAGAGAGAGGGGCTGTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCTGACT CTCTCCTGATGTGGGCCCTCTGTGCTCTTCTCTCCGCTGCTGGGATC
WI-6996	228	T G	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGTCTTTCAGCACCCAGAGGAGGAGAGCCGGCAGTTCCCTGT CAGGAGAGAGAGGGGCTGTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCTGACT CTCTCCTGATGTGGGCCCTCTGTGCTCTTCTCTCCGTCGGGATC
WI-7021b	112	G A	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATGAGCCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTTCGGTCCACATCCACACAGCCAAATCCAAATTAATCAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATGAGCCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTTCGGTCCACATCCACACAGCCAAATCCAAATTAATCAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---	---	GGCAGTAGGACCACAGTGTGGGGTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAA ATGGTGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T	---	---	GGCAGTAGGACCACAGTGTGGGGTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAA ATGGTGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C	---	---	AATTCGCTGAAAAGGAACTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT/C/TCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---	---	AATTCGCTGAAAAGGAACTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT/C/TCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT

WI-7175	194 C T ---	---	CTCCTAGACTAGTGCTTTACCTTTAATGAAGTGTGACAGGAGCCCAAGGCAGTGTTCCCTACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATAATAGTTTACTGCTGTCAATTGTCCATGCCTA/C/TAGAT AATTTATTTTGATTTTGAATAAAACATTTGTACATTCCTGATACCTGGG
WI-7178b	273 G A ---	---	TGTATCAGGTGAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGCTACCTGGCTGCTAGGGGAACAGACCAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTGCTGACATAAGAGAAAATTCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	TGTATCAGGTGAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGCTACCTGGCTGCTAGGGGAACAGACCAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTGCTGACATAAGAGAAAATTCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTA/C/TCTCTCCTCTATT TACTTGAGGCTGCCAATTACCAGCCACGTTTCAGCTCAAGAGATGCCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTGAGCCCTAGTACCCCAATT
WI-7182	106 C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCCA/C/ATCTGAGCCTATCTCTCCTCTATT TACTTGAGGCTGCCAATTACCAGCCACGTTTCAGCTCAAGAGATGCCCTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTGAGCCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACCAGCACCACATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTTAAGCACTCTAGAAACAATGAAGCTCTTGGCATAATTTAAGGAG CTCCCAAAATGIGTTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/C/GGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGGTCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCTTGTCTAA
WI-7199b	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/C/GGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGGTCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCTTGTCTAA

WI-7216c	237	T C	---			TGACACTAACACTCTAATTCAGCGAATGTTGGAACACCACTGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTTTTT/CJCTTGTAATCACIT
WI-7216b	237	T C	---			TGACACTAACACTCTAATTCAGCGAATGTTGGAACACCACTGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTTTTT/CJCTTGTAATCACIT
WI-7220b	147	A T	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA/JTAACTCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGACACATAATTTAGTGTGTTT
WI-7220	140	A T	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC/JTCTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGACACATAATTTAGTGTGTTT
WI-7226	232	C	---			GATCGAATTTTCAGATGATTCGGAAATTTTCATTGAGGTATTTGTAATAGTGACATATATATGTATA TACATATCACCCTCCTATTCTCTAATTTTGTAAATGTTAACTGGCAGTAAGCTCTTTTGTGATCAT CCCTTTCCATATAGGAAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAAAAATAA TTACCCACAATGCCACCAGTAACCTAACGATTCTTCACCTCTTGGGGTTT
WI-7228b	254	G A	---			ATAGCTTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTTACCAGGAGATTACAAATTTTGTCTCTTCTGCTCTTTGTAATCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAAATGTTATCCAACATTTAAGATATCTCAATGTT
WI-7228a	163	G A	---			ATAGCTTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTTACCAGGAGATTACAAATTTTGTCTCTTCTGCTCTTTGTAATCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAA/GAJATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAAATGTTATCCAACATTTAAGATATCTCAAA
WI-7233c	213	C T	---			CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGCTGTTTGTACATCCATTTTCAATTGTTACA GATGTGAACCTTATTCTCTGTCACATAATTTATATTTAAATATTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTTCTGCCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAGTAC/JTGTGCACAAAAACCACTGCCAGATAACCCAGAGGGGCTG

WI-7233b	213	C T	---	CGATCGTACTGCCAGTAGCATTGCTGTGTGTCGGGCTTGTTGTACATTCCATTTCATTTGTTACA GATGTGAACTTTATTCCTTTGTCACATAATTATTTAAAATTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTTGGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGTAC/TGTGTCACAAAACCACTGCCAGATAACCAAGAGGGGCGCTG
WI-7233	211	T C	---	CGATCGTACTGCCAGTAGCATTGCTGTGTGTCGGGCTTGTTGTACATTCCATTTCATTTGTTACA GATGTGAACTTTATTCCTTTGTCACATAATTATTTAAAATTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTTGGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAGT/CJACGTGCACAAAACCACTGCCAGATAACCAAGAGGGGCGCTG
WI-7238	128	T C	---	GCCTACAGACAGCTCACCATTTTGTCTGTATCTGTAACACATTTTGTCTTAGTCTTTCTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTT/CJCCGTT CTGTTTTAAACAGAAATAAAAGGAGTGAAGCTCTTTCTCATTTCAAAGTTGCTACCAAGTGTAT GCAGTAATTAGAACAAAGAAACAATTCAGTAGAACATTTTATGCCTA
WI-7252f	520	T C	---	CCACAGGATCCAGCCAAAGCGGCCCTCCGCCCCCTCCACTCGCAGACAGCCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252e	552	T C	---	CCACAGGATCCAGCCAAAGCGGCCCTCCGCCCCCTCCACTCGCAGACAGCCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252d	540	T C	---	CCACAGGATCCAGCCAAAGCGGCCCTCCGCCCCCTCCACTCGCAGACAGCCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252c	552	T C	---	CCACAGGATCCAGCCAAAGCGGCCCTCCGCCCCCTCCACTCGCAGACAGCCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252b	540	T C	---	CCACAGGATCCAGCCAAAGCGGCCCTCCGCCCCCTCCACTCGCAGACAGCCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCTCTCCA

WI-7252a	520 T C ---	---	---	CCACAGGATCCACAGCCCAAGCGGCCCTCCCGCCCCCTCCACCTGCAGCAGACGCCCGGGACAGAG GCCTGCCCGGGCGCGCCAGCCCGCCCTGGGCTCGAGGCTGCCCGCCCGCCCTGGTCTCTGGTCOG GACACTCCTAGAGAACGACGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	---	AAC TTGGTTATGTCAGTTCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTTCAGATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATATGTAATAATAACGATCTCT AAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCTTT/
WI-7265l	231 T A ---	---	---	AAC TTGGTTATGTCAGTTCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTTCAGATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265k	121 T G ---	---	---	AAC TTGGTTATGTCAGTTCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTTCAGATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265j	174 T A ---	---	---	AAC TTGGTTATGTCAGTTCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTTCAGATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265i	227 T C ---	---	---	AAC TTGGTTATGTCAGTTCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTTCAGATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265h	80 T A ---	---	---	AAC TTGGTTATGTCAGTTCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTTCAGATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265g	170 T G ---	---	---	AAC TTGGTTATGTCAGTTCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTT TTTCAGATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCTTT

WI-7265f	231	T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAAATATAACCGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTT/AJ/AAGGAGTAAAGATTGCGCT
WI-7265e	227	T C ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAAATATAACCGATCTCTT AAAAATACCACAGTTTGTATTTT/CJ/CITTAAGGAGTAAAGATTGCGCT
WI-7265d	174	T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265c	170	T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265b	121	T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265a	80	T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTT/AJ/ATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAAATATAACCGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7281b	183	C ---	---	---	GATACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGCGAGGCCGAG GTGTTGTGAAGACCACCTGTTCTGTGGTTGGGGTCTCTGCAAGAGGCCCTCTC
WI-7281	171	C A ---	---	---	GATACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTC/AJ/TTGGCAAAAACGGAGTCCGCGAGGCCG CAGGTGTTGTGAAGACCACCTGTTCTGTGGTTGGGGTCTCTGCAAGAGGCCCT

WI-7301	205 A C ---	---	---	AACTATGGCAGTGGTCTCTGTTATAGTAGAGGGGGTATGGTGGTGGACCATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGAGGATATGATGTTACAAATGAAGGAGGAAATTTGA CGGTAGTAACATGTTGGTGGGAACATATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTAC/TGGACACATGAAGGGGGCAGTTTGGTGGAGAAGCTCGGGCAG
WI-7314c	49 G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTCGGTTTAAATTTGGGAGGTCA/GA/TGTCTACCTCACTG AGAGGGAACAGAGGATATGCTTCTTTGACGAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314b	49 G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTCGGTTTAAATTTGGGAGGTCA/GA/TGTCTACCTCACTG AGAGGGAACAGAGGATATGCTTCTTTGACGAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314	36 A G ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTCGGTTTAA/GTITGGGAGGTCA/GA/TGTCTACCTCACTG AGAGGGAACAGAGGATATGCTTCTTTGACGAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACTATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7321b	199 C T ---	---	---	ACTCAGGGAAGGATGCCCATTAAGTGACAAAGGGTGGGTGGCCACCATTGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCCATC/C /TGTGTCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---	---	---	ACTCAGGGAAGGATGCCCATTAAGTGACAAAGGGTGGGTGGCCACCATTGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCCATC/C /TGTGTCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---	---	---	AGACATTCCTGCTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAGTGGGCACATGCTCAGGCTACTATAGTCCAGAAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTAAATCTGAATTTGGGATTTTCAAAAGATAATTTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA/A/C/A
WI-7338c	221 A G ---	---	---	CTCTTCTCAGCACATTGATGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGTACATGCCAATGATAGGTGCAAGAATATGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC/A/G/TATACACACAGACATCAGAAATTCGTGT

WI-7338b	125 A C ---	---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTGCTTTA/C/CCTTG AGCCATTATTTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	125 A C ---	---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	221 A G ---	---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTAATTCATTGTAACAGGTAATTTCTTCA CAGATCTCATTTT/A/JAAAAATCTTAATGATTATTTTATTACTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACATACATTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384c	146 T A ---	---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTAATTCATTGTAACAGGTAATTTCTTCA CAGATCTCATTTT/A/JAAAAATCTTAATGATTATTTTATTACTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACATACATTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146 T A ---	---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAAATTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTAATTCATTGTAACAGGTAATTTCTTCA CAGATCTCATTTT/A/JAAAAATCTTAATGATTATTTTATTACTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACATACATTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145 T A ---	---	---	TGAAATCCTGGTCTCTGGCTGCTGCTAGCTGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAACTGTAAGCGACT/A/JTAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTGA CTTGTTCTGTCCCAAGAACTTTCCCCCAAGATGTGTATAGTATGG
WI-7388c	106 A T ---	---	---	TGAAATCCTGGTCTCTGGCTGCTGCTAGCTGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAACTGTAAGCGACT/A/JTAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTGA CTTGTTCTGTCCCAAGAACTTTCCCCCAAGATGTGTATAGTATGG
WI-7388b	106 A T ---	---	---	CTTGTTCTGTCCCAAGAACTTTCCCCCAAGATGTGTATAGTATGG

WI-7388	94 T A ---	---	---	TGAAATCCTGGGTCTCTGGCCCTGTCTGTAGCTGGTTTATTTTACITTTGGCCCCCTCCCCACTTTTTT TGAGATCCATCCTTTATCAAGAAGT/AJCTGAAGCGGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCAATTGCAACAAGGTACCTCTATTGGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTGTCTCCAAAGAACTTTTCCCCCAAGATGTGTATAGTTATTGG
WI-7438	64 A G ---	---	---	TTAGATTTTAATTGGCAACCAAGCACTCACTGCCACCATCCACTGCAGATCTNCTATTCTCTGG(A/G) GTTGATATGACAAAGAAACCCCTATTGGAACCAAGTCTTCAGATTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTACATGTACACTGTACTGTCTCACTGTAAACATAGTTGTGTCGTTATTTGTTA TTGGAATGAATATCGCTTCCACTGACITTTACCA
WI-7454b	152 T C ---	---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7454	152 T C ---	---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAAATGGCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7464c	177 G C ---	---	---	AATTTGAAAACTCTGAAAAAAGTGCAATAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACATAAATTACTATTATAATTTCTATGTA CAACAGAGCCACAGCACAGAGGGTGGCATAGCAGTTGCCA/GC/CAGAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCAACCAAAATTAT
WI-7464b	168 C A ---	---	---	AATTTGAAAACTCTGAAAAAAGTGCAATAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACATGCACATAAATTACTATTATAATTTCTATGTA CAACAGAGCCACAGCACAGAGGGTGGCATAGC/AJAGTTGCCAGCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCAACCAAAATTAT
WI-7464a	103 C A ---	---	---	AATTTGAAAACTCTGAAAAAAGTGCAATAGCAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAAATG/C/AJACTAAATTACTATTATAATTTCTAT GTACAAAGAGCCACAGCACAGAGGGTGGCATAGCAGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCAACCAAAATTAT
WI-7499b	134 T G ---	---	---	CAATTCCTCAATCCAACTAGTCTGTGTCCTAAACCATTCAGACAACTTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGCTTCTTTGAATGCTTCAIT /GJTATAGTCCTCTTCATTTAGCAATCAGTGAAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAATCCCTTTGAAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A ---	---	---	CAATTCTCAATCCAACCTAGTCTGNTGCCTAA/JGCCATTCCAGACAACTCCACTTCGAAGGTTTAAATGCATAAGTCAGATAGCAATCCTTCAGTTCGCCAGAGGCACATCACGTTCTTTGAATGCTTCATTATAGTCCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTITTAGGAACTCTGTACAAAAATCCCTTTGAAATATATAAATTTTGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAATGCATCCAGCAGCAGACCACTTNAAGTAGTCTGCTGCTGATTGCCTAGC/A/CJGGAGAGTTGAGTGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCAGAAGAAATATTTTAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAATGCATCCAGCAGCAGACCACTTNAAGTAGTCTGCTGCTGATTGCCTAGC/A/CJGGAGAGTTGAGTGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCAGAAGAAATATTTTAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 CT ---	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTTCTTGATGTTTCGAGTGCACCCCAAGAGTCAGAACTGTACATCCCAAAATTTGGTGCCGTGGAACACATTCGCCGTGATAGAATTGCTAAATTGTC/TGTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTAAATTTGGATTGGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTTCTTGATGTTTCGAGTGCACCCCAAGAGTCAGAACTGTACATCCCAAAATTTGGTGCCGTGGAACACATTCGCCGTGATAGAATTGCT/CJAAATTCGTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTAAATTTGGATTGGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAGTCCTGTTTGACGGGAAGCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTTGACTTGAAC TAGATTGCATGCTTCCTCTTTCCTTTG/AJGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAGTCCTGTTTGACGGGAAGCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTTGACTTGAAC TAGATTGCATGCTTCCTCTTTCCTTTG/AJGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/TCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGATTCCTGTTAAAGCCACTTGGGTCATAAGAAAGGGAAGTAAAAAATGAAGTCTGACTAGAAAATCTATTGCAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTTCATTTCATTTGATGTGCAATTTGAATTCAG

WI-7555b	60	T C	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTTCJCTTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTTGGGTG ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTTCAG
WI-7555	60	T C	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTTCJCTTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCCTGCATTCCTGTTAAAGCCACTTGGGTG ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTTCAG
WI-7567b	290	G T	---	TGAGCCATCACTAGAAAGAAAGCCATTTTCAACTGCTTTGAAACTTGCCTGGGGTCTGAGCATGAT GGGAATAGGGAGACAGGGTAGAAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCCTTGG ATCGCTAAGCTGGCTGTTGATGCTATTATGCAAGTTAGGTTCTATGATTTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCCCTTGGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T C	---	AATGTATCCCCCTTCGGTCCAACAACAGGAAACCTGACTGGGCAGTGAAGGAAGGGATGGCATTCJ AGCGTTATGTGTAAAAACAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAAGTGAATCCAT TGCGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAATAGCGTTGTTATCGCCTTGGGTTTAAAT ATTGATGAGTTCCACTTGTATCATGGCCTACCCGAGGAGAAGAGGAGTTTG
WI-7574c	216	A G	---	GCCACAGCAAGTGGAGCGGTGTGAGGAAGGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCATTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCAGGGCAGTCTGCTGGCTGACCAGTTACTATCCCGTTA
WI-7574b	216	A G	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCATTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCAGGGCAGTCTGCTGGCTGACCAGTTACTATCCCGTTA
WI-7574	216	A G	---	GCCACAGCAAGTGGAGCGGTGTGAGGAAGGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCACTCTCGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCATTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCAGGGCAGTCTGCTGGCTGACCAGTTACTATCCCGTTA
WI-7576c	168	A T	---	AATGATGATGATAATGATGATGACGACGACAAACGATGATGCTTGTAAACAGAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAAAACTGGCATCTGACACAAAAAAATGTTGTTGAAGGCCCTTATTCTACATTTCCACCTAC TTTGTAGTGAGAGAGACAAGCAAGCAANNNNNNNNNNAAGAAAAATAAAC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAGACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA TAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA TAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117 A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTATTCTTTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACAGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTAATTC
WI-7577	107 G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTATTCTTTCTCTGAG/GJATTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACAGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATGACTGTAATTC
WI-7619q	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGGTCATCCCTCCCTAACGAGACTC/GJCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTC/GJCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACAT/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90	C G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206	T G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCT[G]TTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106	C G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150	T C	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228	A G	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATTA[G/C]ACATACCGAGAAACCTATTTC
WI-7619f	237	G C	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTCTTACACAGAAACATACATACC[G/C]AGAAACCTATTTC
WI-7619e	99	C T	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T A	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	ACAGGCGACTTGAAGAGGACGCGAGGCTTCAGAGGACAAACCCCAATACAGGAGAGCAAGACAGAC AGAGAGGGCCAAATGGGGTCATCC/G/GCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAGGCGACTTGAAGAGGACGCGAGGCTTCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC/T/GTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAGGCGACTTGAAGAGGACGCGAGGCTTCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAGGGCCAAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATGGGATCTGTCTGGC/G/GTTAAACCATCATGGACCAATGTG CCATACATATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
WI-7626c	155 C T ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAATGTGCCA TACTAATGATGAGCATTTAG/C/TJACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
WI-7626b	28 T A ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTJ/JTTAAATATATGTATTTAAACAAAAAGCAACAG TAATCTATGTGTTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAATGTG CCATACATATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
WI-7626	144 T C ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAATGTGCCA TACTAATGA/T/CJGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
WI-7689c	134 A G ---	---	TCCCATAACCGCTGATTCTCAGGGTCTCTGTGCGCCCAACCCAGATGGGGAAAGCAGAGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCGAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTTGAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134 A G ---	---	---	TCCATAACCGCTGATTCACAGGTCTCTGCTGCGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGGAAAGGTTGTTCCATAA[A /G]TAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A ---	---	---	TCCATAACCGCTGATTCACAGGTCTCTGCTGCGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGGAAAGGTTGTTCCATAA AATAAGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A ---	---	---	TGGAGAACATTCAATCTTCCGTCACATTTCATCAATGAAGATTAG[A]CACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCCACAGCATGGTAGTGGCAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGAGGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACTGTCAGTTCAATCC
WI-7703b	164 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGTTTTCACATTGGAAACAAAGTCAGTCATTAGATATGATTCAAA TGCTATAAACCAAACTGATGAAGTAAATTCJGGTCTCTCAGTTGTTTATTTAACCTCTAAATCTCT TTCATTTTAGGGTAGCATTTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGTTTTCACATTGGAAACAAAGTCAGTCATTAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAGTAAATGGTCTCTCAGTTGTTTATTTAACCTCTAAATCTCT TTCATTTTAGGGTAGCATTTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGAGGCCAAGG GTTACAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGAGCCTCATCCAGGCAAGGTCAGGA GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGAGGCCAAGG GTTACAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGAGCCTCATCCAGGCAAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGAGGCCAAGG GTTACAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGAGCCTCATCCAGGCAAGGTCAGGA GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCACG

WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGGAAGACTGTGGTCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTACTGGGGTCTCTGGGGCTCGAGCCTCATCCGAGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGGAAGACTGTGGTCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGGCTCGAGCCTCATCCGAGCGAGGTCAGGAGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGGAAGACTGTGGTCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTACTGGGTCTCTGGGGCTCGAGCCTCATCCGAGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGGAAGACTGTGGTCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGGCTCGAGCCTCATCCGAGCGAGGTCAGGAGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGGAAGACTGTGGTCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTACTGGGTCTCTGGGGCTCGAGCCTCATCCGAGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGGAAGACTGTGGTCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGGCTCGAGCCTCATCCGAGCGAGGTCAGGAGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGGAAGACTGTGGTCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTACTGGGTCTCTGGGGCTCGAGCCTCATCCGAGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAAACACTTACAGAAATATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGCTTTCAGAGACTTCGTAAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[A/G]TAGTTTAAAGTGCATTATAAATTTTATACAGAAATTAAGTAGATTTTAAAAA GATAAAATGTGTAATTTGTTTATATTTCCCAATTTGGACTGTAACGACTGCC

WI-7765b	126 G C ---	---	ACAGGGCCTTTGGCAGGTGCAGCCCCACCTGCGCTTTGACCTGGCTCCCTTCATGCATGGAAATCCCT TCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGG GAAACATTCCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTGCACCCCTCATGCTGTGTG ACTCAACCAAAATCACTGAACCTTGTGAGCCTGTAAAATAAAGGTCGGA
WI-7773b	237 C G ---	---	TTAATTTACTGATCCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTATCCGTAGTTTT GATAAAGATTTTCTATCTTGGTTCTGTGAGAGAACCTAATAAGTGTACTTTGCCATTAAAGCA GACTAGGGTTCACTGCTTTTACCCCTTNNNNNNNNNTGAAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170 T C ---	---	TGCAACCTCTTTTCGTATGGGAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGAGCGGCCACCCAGAAT CAGATCCCAGCTTCGGCATTGTATCAGACCAACAGTGTCTTCCCGGGAGGAAACACTTTTAA TTACCCCTTTTGCAGGCACCACTTTAATCTGTTT[C]ATACCTTGTATTAAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCTTGTAGTCAAGTAAATGIGCTTGCT
WI-7785c	165 G -- ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCAATTGGAATAAACTGTCTCCCCATTGCTCTATGAACTGC ACATTGGTCAATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATACATTTACCA TAATTTATTTGTCCATTGATGTATTATTTTGTAAATGTATCTTGGTGTGC
WI-7785b	165 G -- ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCAATTGGAATAAACTGTCTCCCCATTGCTCTATGAACTGC ACATTGGTCAATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATACATTTACCA TAATTTATTTGTCCATTGATGTATTATTTTGTAAATGTATCTTGGTGTGC
WI-7785	156 - T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCAATTGGAATAAACTGTCTCCCCATTGCTCTATGAACTGC ACATTGGTCAATTGTGAATANN[/T]NNNNNNNGCCAAAGGCTAATCCAATTATTATACATTTACCATAATTTATTTGTCCATTGA TGATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84 G A ---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTTACAGAGACTCTCC TGACGGTGGAAATTAAG[A/TT]TAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAATCGGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT
WI-7789b	84 G A ---	---	TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTTACAGAGACTCTCC TGACGGTGGAAATTAAG[A/TT]TAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAATCGGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT

WI-7789	73 G A ---	---	TCTCCCCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTAAGTTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190 C T ---	---	AATTGCAGTCACCTTCTTCAAAACCTTACAGTCCCTCCTAAGGTTACTCTTCATGAGATTATCCATT TACTAATACCTGATTTTGGTGGACTAGGCTTGCCCTATGCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190 C T ---	---	AATTGCAGTCACCTTCTTCAAAACCTTACAGTCCCTCCTAAGGTTACTCTTCATGAGATTATCCATT TACTAATACCTGATTTTGGTGGACTAGGCTTGCCCTATGCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 C A ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATCTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7795	81 C A ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAAATCTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7814c	41 G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814b	41 G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814	28 G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]CATGCCAGTCCCCTTTTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---			GCAGGAATAGTCACTCATCCACTCCACATAAGGGTTAGTAAGAGAAGTCTGTCTGATGA TGATAGGGGGCAATCTTTTCCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTAGT[C/TTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTTGTTTTCGTGCACATTTTACTTTTTTGGGTGGGA
WI-7830c	54	G A	---			GCAGGAATAGTCACTCATCCACTCCACATAAGGGTTAGTAAGAGAAGTCT[G/AT]CTGTCTGA TGATGGATAGGGGGCAAAATCTTTTCCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAAATTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTTGTTTTCGTGCACATTTTACTTTTTTGGGTGGGA
WI-7830b	134	G A	---			GCAGGAATAGTCACTCATCCACTCCACATAAGGGTTAGTAAGAGAAGTCTGTCTGATGA TGATAGGGGGCAATCTTTTCCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC[G/AT]CCATAACTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTTGTTTTCGTGCACATTTTACTTTTTTGGGTGGGA
WI-7830	44	A G	---			GCAGGAATAGTCACTCATCCACTCCACATAAGGGTTAGTAAGAGAAGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAAATTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTG AGTTGATCGTTGTTGTTTTCGTGCACATTTTACTTTTTTGGGTGGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/TTAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/TT]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCCAG[C/TTAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGG ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/TT]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	CCACTTCTATCTGATTTTCCCAG[C/T]AATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	CCACTTCTATCTGATTTTCCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	TTCAACACCTGTCTCCACCCTCCACCCTCTGTGCAATCACTTCCACCCTCAGCCTCAGCTAGTCCCC CTAACAAATACCCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGTTTAAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGTCTATAAATCTATGT CTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ---	---	TTCAACACCTGTCTCCACCCTCCACCCTCTGTGCAATCACTTCCACCCTCAGCCTCAGCTAGTCCCC CTAACAAATACCCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGTTTAAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGTCTATAAATCTATGT CTATATGTCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTCCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCAACCTGCTCCCTGTATCCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACACAAT CATTTAATTTCCCTGTCTTACCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTCCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCAACCTGCTCCCTGTATCCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACACAAT CATTTAATTTCCCTGTCTTACCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCTAGAT
WI-7868	66 T C ---	---	TTGATCGATCTTTCCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT /C/TCAACCAACCTGCTCCCTGTATCCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACAC AATCATTTAATTTCCCTGTCTTACCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCTAGAT
WI-7870b	85 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTATTAGAAGGG GTGGGGTGGCGGGAATCC[C/T]ATTTATCAGACTCTGTAAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAAGG GTGGGTGGG[C/T]GGGAATCCTATTATCAGACTCTGTAAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATGGCTGCAAAAATGAAATCCAATGAGCACTAGAATATTTAAACATCACTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCGGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCTCCCAAGGCTGCTCTCCAGAGCAACAAG
WI-7889b	54 C ---	---	---	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCGGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCTCCCAAGGCTGCTCTCCAGAGCAACAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCCAATATACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[AG/T]ATGTAAATTTGCATTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCCAATATACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[AG/T]ATGTAAATTTGCATTTTTTATTGAAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC

WI-7900d	128 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAAGTGATTAAAGTTTGGATCAAGCCCATGGTGA[C]/TACA AAATGCAATTGATCATGAATAGAGGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAAGTGATTAAAGTTTGGATCAAGCCCATGGTGA[C]/TACA AAATGCAATTGATCATGAATAGAGGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAAGTGATTAAAGTTTGGATCAAGCCCATGGTGA[C]/TACA AAATGCAATTGATCATGAATAGAGGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAAGTGATTAAAGTTTGGATCAAGCCCATGGTGA[C]/TACA AAATGCAATTGATCATGAATAGAGGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAAGTGATTAAAGTTTGGATCAAGCCCATGGTGA[C]/TACA AAATGCAATTGATCATGAATAGAGGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAAGTGATTAAAGTTTGGATCAAGCCCATGGTGA[C]/TACA AAATGCAATTGATCATGAATAGAGGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T ---				AGACTTAGGTACAATTGCTCCCTTTTATATA[C]/TJAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTGGGTCGCTGGGTTATGGGCGAGCGCCGCTGGTCT CACTCAGTCGCTGCATGCTCTGTCATACAGACAGGTAACTTAGTTCT
WI-7901b	33 C T ---				AGACTTAGGTACAATTGCTCCCTTTTATATA[C]/TJAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTGGGTCGCTGGGTTATGGGCGAGCGCCGCTGGTCT CACTCAGTCGCTGCATGCTCTGTCATACAGACAGGTAACTTAGTTCT

WI-7901	33 C T ---				AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATGTCATCTATTTTCCATATAGTCATCAAGAGACCATTATTAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTTGTTGGGGTGGCTGGTTATTGGGCAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G ---				AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTCATGTCATCTATTTCCATATAGTCATCAAGAGACCATTATTAACATGGTAAGACCT TTTTAAACAACTCCAGGCCCTTGTTGGGGTGGCTGGTTATTGGGCAGCGCGGTGGTGGTGCAC TCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCTG
WI-7926c	150 C A ---				CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTAAGCAAAAGTGATACAAACACAGTATTTGGGAATGCCCTTCATT TACAATGCAATACCTA[C/A]ATTTTAACTCTTGTAGGAGAAAGCAACTGTATAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926b	28 A T ---				CATTCCGCATCTGTCAACAGGACAGAAATGTCATGGACAAGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAATTCATATTAAGCAAAAGTGATACAAACACAGTATTTGGGAATGCCCTTC ATTTACAATGCAATACCTA[C/A]ATTTTAACTCTTGTAGGAGAAAGCAACTGTATAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926	150 C A ---				CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAATTCATATTAAGCAAAAGTGATACAAACACAGTATTTGGGAATGCCCTTCATT TACAATGCAATACCTA[C/A]ATTTTAACTCTTGTAGGAGAAAGCAACTGTATAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7947b	203 G T ---				AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCATTAAGCAGCCAGACCCACAGGCCAGGTCTGT GCTATCAGAGGTCACTCTTTACAGTTAGAAACACAGCCAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]CTCTCCCTGGAGCAGCAGACTATGGCAGCCAGTCTGCCACCTG
WI-7947	203 G T ---				AAGAGCCAGCAGGTCAAAAAGGCCAACACAAACCATTAAGCAGCCAGACCCACAGGCCAGGTCTGT GCTATCAGAGGTCACTCTTTACAGTTAGAAACACAGCCAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]CTCTCCCTGGAGCAGCAGACTATGGCAGCCAGTCTGCCACCTG
WI-7963b	145 T C ---				CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAAAGTAAGACTAATTTTAAAAATAAAATGCC ACAAATTTCAATTTCTCCTTCAAGTATTACAATGGAGTTTATCTCGCTTAAAGTGAAGAAAT TGAGTGAATGA[T/C]AATTTTGAATTTAGGATAGATCCAAGTTATTTCCCAACTCTTTTCC CCATAAAGTTAGGATGAGGAGGAGCACTATTAAAGGCAGAGACGGGAAA

WI-7972c	268 T G ---	---	GGAGTTCTGGTTCTACTGGGGCAACCCCTGGTGACCAAGCACCATCTCTCTCTCTTTCACAGTTCTCT CCTTCTCCCGCTGTAGCCATTCTCTGTTCCCATGAGATGCCATGGTCTCAGCAGGGGAGG GTAGAGCGGAGAAAGGAGGAGCATGCGGGCTTCTCTGGTGTGAAGAGCTCCTTGATATCCT CTTTGAGTGAAGCTGGGAGAACCAAAAGAGGCTATGTGAGCAACAAGGTA
WI-7972b	268 T G ---	---	GGAGTTCTGGTTCTACTGGGGCAACCCCTGGTGACCAAGCACCATCTCTCTCTTTCACAGTTCTCT CCTTCTCCCGCTGTAGCCATTCTGTTCCCATGAGATGCCATGGTCTCAGCAGGGGAGG GTAGAGCGGAGAAAGGAGGAGCATGCGGGCTTCTCTGGTGTGAAGAGCTCCTTGATATCCT CTTTGAGTGAAGCTGGGAGAACCAAAAGAGGCTATGTGAGCAACAAGGTA
WI-7972	268 T G ---	---	GGAGTTCTGGTTCTACTGGGGCAACCCCTGGTGACCAAGCACCATCTCTCTCTTTCACAGTTCTCT CCTTCTCCCGCTGTAGCCATTCTGTTCCCATGAGATGCCATGGTCTCAGCAGGGGAGG GTAGAGCGGAGAAAGGAGGAGCATGCGGGCTTCTCTGGTGTGAAGAGCTCCTTGATATCCT CTTTGAGTGAAGCTGGGAGAACCAAAAGAGGCTATGTGAGCAACAAGGTA
WI-7981	261 T G ---	---	AACCCCTGAATCGGAAGGGACITTCCTCTTCTCTCTCTTCCCTGTTTAAATATAAGATGTCAT CCCTTGTGCAGACAGACCCCTGGCTTTTCTTGGCAGAGAGGACCCACTGGACTGGGTTTTG TCTCTGCATCTCATTGTAGAGCTTGGTGGCTGAGCTTGGCCCTATTAAAGATAAATAGAGTTCCAAATA AGGATTGTTACATGCATCATATAACCATTCCTCCATTGGTCTCCTAAAACAT
WI-7992b	62 A G ---	---	GAGCTTCACAGTGAAGATGGAGAAGGTGAACTTGCTTTGAATATNCCAGATTTGTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTTCTTTCACGAAAATTAAATGCTATCAAGAGCAAAAC TATGAACATTATATCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACITTGCAATTGAACATTCC AGATGTGTGAGATCATGTGATTGTCAGTGGCAGGTATTGCTTTGCTTGC
WI-7992	62 A G ---	---	GAGCTTCACAGTGAAGATGGAGAAGGTGAACTTGCTTTGAATATNCCAGATTTGTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTTCTTTCACGAAAATTAAATGCTATCAAGAGCAAAAC TATGAACATTATATCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACITTGCAATTGAACATTCC AGATGTGTGAGATCATGTGATTGTCAGTGGCAGGTATTGCTTTGCTTGC
WI-8004b	183 C T ---	---	ACTAAGAAATATTTATGGTGGCCTATAAAACCTGTTGAGTCTTACCTTGTCTAATGATTTATTTT CATTAAAGTAAATGATCATCTTTGGGAGGCATTTTATAAAAACATATTTAGGAGAAAATTTCTTTGA TTTATGCTATAAGGTAATGTTCATAATTTCTTGCCATGTGAATTG[C/T]AGGTTTCCACTTTGAG AGAAATCTCTCAATCTAATAAAGACCAAGGCCAGAACACTAAGATA
WI-8021c	57 C T ---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCATCTCTGAAA[C/T]GATCCC ACGCTTAGAACCTTCACCAAGGAGTTTTCTTGTAGTATTCTCAAAGCTTGTGAGGCATTCGA ACTGGTCTTTCACITTTGAGATCTTTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTGGAATCGGTTGATTTGCCA

WI-8021b	57 C T ---			ACAATCTCAGAAAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATTCATCTCGAAAC[C/T]GATCCC ACGCTTAGAACCTTACCACAAGGAGTTTCTTGAGTGAATCTCAAAGTCTGGTAGGCATTCGA ACTGGTCTTTACATTTGAGATCTTTCTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGIGATTGGAATTCGGTGAATGGCA
WI-8021	57 C T ---			ACAATCTCAGAAAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATTCATCTCGAAAC[C/T]GATCCC ACGCTTAGAACCTTACCACAAGGAGTTTCTTGAGTGAATCTCAAAGTCTGGTAGGCATTCGA ACTGGTCTTTACATTTGAGATCTTTCTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGIGATTGGAATTCGGTGAATGGCA
WI-8024c	206 A G ---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTACAGGAGGACAGGGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAAAGAGAGT GGCCCCAGAGATGGAAAGGACCCAGTGTATCACCACAACCACTTCAGCCGCTTAGCCTCTAA TTCCCA/G/CTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAAGGAAAGAGC
WI-8024b	206 A G ---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTACAGGAGGACAGGGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAAAGAGAGT GGCCCCAGAGATGGAAAGGACCCAGTGTATCACCACAACCACTTCAGCCGCTTAGCCTCTAA TTCCCA/G/CTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAAGGAAAGAGC
WI-8077	167 A G ---			GAATGAGCCTTCTAGCGCCGAGGGAGCTGCTGCTGTTGTTGGCCTGCACATGCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACCTCTTCT AAGGAGCTGGGGTGTATGCCCTACAAACCC/G/CTAAATCTCATCAGATGGATTTTATTAAACGTT GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGAAAAA
WI-8118f	114 G C ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTTCGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTTCGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTTCGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGAC/TGCACTCCCTTGCTAAGGAAGC TATGTACTTTCATGCTGTGGAACCTGGCAATACAGAATGTAGCTTGTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAC/TGCGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---	---	TTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAAGTGGCAAGAGACACAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8171c	46 A G ---	---	TTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGGGAAG AAGAGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGAGGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGACACAATGAAGAGGATGATATAAAACAATCAC
WI-8171a	46 A G ---	---	TTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGGGAAG AAGAGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCAC ACATTTATGAGGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGACACAATGAAGAGGATGATATAAAACAATCAC
WI-8171b	298 T C ---	---	TTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAATGGCAGCGGGCCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAAGTGGGCAAGAGACACAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8314b	85 G C ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTAAGGG/GC/JAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAAGAGCACTGTCCAATAGAACTTTC TGATGATGATGAAAAGATTCTACTCTGACCTATTCAATAGGGGTAAACCACT
WI-8314	78 C G ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAAGAGCACTGTCCAATAGAACTTTC TGATGATGATGAAAAGATTCTACTCTGACCTATTCAATAGGGGTAAACCACT

WI-8321	178 G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATCTAGTCTGAGTCTGAGAAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGATG/AJAGTATCTTAGTATCTTTCTA TTTGCTATGGTCTAGTTATCAACCTACTTTAATAGCTGAACGTGTTGGC
WI-8321	178 G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATCTAGTCTGAGTCTGAGAAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTCTAGTTATCAACCTACTTTAATAGCTGAACGTGTTGGC
WI-8332b	123 A C ---	---	---	TATGTAACCTACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCAAAGCCCGAGTCTTCCCTCCCTGTCAGCCTTAGA/CJACTAAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCGAGCAATGCCTACTGCGAGCTACTAGTAAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114 A C ---	---	---	TATGTAACCTACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCAAAGCCCGAGTCTTCCCTCCCTGTCAGCCTTAGA/CJACTAAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCGAGCAATGCCTACTGCGAGCTACTAGTAAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311 T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAGCGGAAGG GGAAGCAAGGACCTTCTACATGGCAGCAGGAGAAAGAGAGGAGGAGAGTCTACACACTTTT AAACAACCATGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCTCCCAACACGTGGGG
WI-8378	308 T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAGCGGAAGG GGAAGCAAGGACCTTCTACATGGCAGCAGGAGAAAGAGAGGAGGAGAGTCTACACACTTTT AAACAACCATGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCTCCCAACACGTGGGG
WI-8426	184 T G ---	---	---	TTTAGCACATATTTAGCATTAAAGCTCAACGATACAGCAATATGTTACATTCTCTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACCTCGACTGTGCTTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTGTGGANGGGGTGGCTTTGCTTGAACCTCCATTCTGT/GJGCTTGTAGCTGGTG AGGCTGGAGTATGGANGGNCCTGGGGGCTTGGNATNGNATTCAGTGAG
WI-8450h	61 C A ---	---	---	TTGAGCCTCCACAATAATGCAACCAAGTTTACATTTTAAACAGCCCTCTACATACACTC/AJCA TCCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTAAGA AAAAACCTTCCAGTTATTGTGCAAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT

WI-8450g	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCAGTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCAGTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCAGTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCAGTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A/G ---				CAAGGAAAGCTGTCAGTCTTCATAAATTTCAAGAGTTACAAAAATACGTATTTTAA/JGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGTACATTCGTACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATAGTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAGCAGCTGAGCAGAGTCTCA

WI-8461c	105 A T ---				CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGNTTAAACAATTAACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---				CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAAT[C]ATAACTACAACCTTACAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCAATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGNTTAAACAATTAACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---				CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGNTTAAACAATTAACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---				CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGNTTAAACAATTAACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---				AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGTACCTTAATTTTGTATAAAAAAAT TAAAAGCAT[A/G]AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTC TGCTCAGTAATTAATAATCTCCCTTTGTTTGTCTTTTAAAAAACATTATTCTGAAAAA ATCAGAAAAACATGATCGTGAGAGAAATTATTA
WI-9439b	101 C T ---				ACAGAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAATCCCAGTCTGCAGCTCAGTACCTG[C/T]GTGCACACTGTACCATCTCAGTCCCCTCT GCCTGTAACCTTAGAAACAGCCCTACCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTGCTGAGCTAGAAAACCTTGACCTGTAAAAACAAAG
WI-9439a	76 C T ---				ACAGAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAT[C/T]CCAGTCTGCAGCTCAGTACCTGCTGTGCACACTGTACCATCTCAGTCCCCTCT GCCTGTAACCTTAGAAACAGCCCTACCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTGCTGAGCTAGAAAACCTTGACCTGTAAAAACAAAG
WI-9446b	75 T C ---				GAAAGCTTGATTAAAGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[C/C]CTCTAAAGNACACATGCCCCAAATGACCCANGNCAAGCAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTCNCCCTACTNTTATCACTGTGCTCTCTGCTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAAAGGGAGGNTTATTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT/CICCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTTTCATATATGTGTGTTGTNCCCTACTNTTATCAGTGTCTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATCTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTCTCTAGATGAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTCTACATGGAAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATCTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTCTCTAGATGAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTCTACATGGAAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAAGTTTCTATTTCATCCATCACAATAGATTGTGCTAAGGATCATTTTGGGAAGATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTTGTA/C/AJAGTG AAAGCTTTCAGCTTGGAAACAACCTTGTCAGGCGAGCTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAAGTTTCTATTTCATCCATCACAATAGATTGTGCTAAG/G/AJATCATTTTGGGAAGAAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCCAGCCATGATCTATGGTGATTTTCCACACATTTGACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGCTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGTATCTGCTTTCAGTTTGTATTGTACAATGCTGTAGATAATGAGGCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GT/C/GCTGGATACCACTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	CCAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/G/AJCTTGAANAATCAATTTCAAGGGACTCTTTTAAATCA GTTAAATAATCTGCTTTAGAAGGCCACAAATGATCATACITTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNCCTTCACATTTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTCTGGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAACTAGGGTTGTGGACAAGTTACTCTCTA/TGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACACTGCACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACCTTGGAAAAAATGACGCACA TAAGTATCATAACTGAGGGTTGGGACAAAGTTACTCTTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATCAAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCCTTTCA ACATCTTTGTACATTTTAGGTGATGCTCTTTGTAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACTCTGTCCTTTACCTGATACATTTATTCATTTACTTTCACTTGGATTTTAAAAAATGTTA ACTTAATACGCTCTCTCAGATGCCCTGCTTTTAGTTAATGTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTTGTTT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTTGTTT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTTGTTT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA CTTCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTTGTTT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTTGTTT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTTCTGCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC[C/A]TTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGAGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTT[O]CCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCCCC[C/A]TTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGTATTCCTGGTGCCTGTGTATC/AJATTACAACTCATTTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTTCAAAACAGTAATGAGTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTCTGTGACCTTGCCTGGAGCGGGTGTCTTCACTATGTGAGTATCTA TCCTTTTATTTCTGTCCCTTATGTTGGTGGCACATGCTGTATTGCTGTCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGTATTCCTGGTGCCTGTGTATC/AJATTACAACTCATTTGATCACAATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTTCAAAACAGTAATGAGTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTCTGTGACCTTGCCTGGAGCGGGTGTCTTCACTATGTGAGTATCTA TCCTTTTATTTCTGTCCCTTATGTTGGTGGCACATGCTGTATTGCTGTCC
WI-9756	47 A ---	---	ACTGAAATGTAAATGGCAAGGACCCAGGACCTTAAATCAATAAGAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGTGTATGTGCCCTTATCACTTTAGTC AGTAAAGATAAGAAAGCCCTGTGTGAGTATCCACTTCCACAACACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCACTTGATTCTTCACTTTTATGATTTAAACTCTCCGTGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTGCAATTGTTAATGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAAGAGAAATCTTGTTCGCAAGGTCAATTTTATATACTATTTA A/A/GJTAAATAACTCTGGTAGGTTCTATAGCAATGCTAAGTAAAGTAAACCGCTGGTTTCTAAATT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCCAGGCAGCGGGGAAAATGGATACTTTCATATGTCTGTACCCCACTATAAACTTTTG GTTCTCATGCACCATTTTCATTTTGCCCTTCTACTCCAAGTACCAGTATTTTACCAATT[G/A]CTCTC ATAATTGACTTTTGTACTGGAAGAAACTCTTAGAATGTTGGAAATTTCTCTATTACACACTTTGCCTCA AAGAAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCCTCCCTTTGCTCCTCATGCCACCTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTT[C/A]JTGATCCACCCAGGA CTCAAAAAAAGTAAAGTGGGAGAGAGGACCTGGAATCGGTGTGCTAGCAAGCCCCCAGGTGG TTGTAAAGTGGACTAAAGTTTGAGGACCAAGACATGGAAGGTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATCCATTTTGAATGAAATAAAATAC/AJGTGTGTATGATATATATCTATTAAACACTT AGGATTATATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTGTTACTTGATATGCTGTG
WI-9880c	222 G A ---	---	GAACTAACACCTTCTTGCTGATGTTTCTTGATTATGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCCTTGGACTATATAAGATCCCTTTTAAATTTATATTTATATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATACCTACATATTTTG

WI-9880b	157	C A ---	---	GAAC TAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTTATGATATCTCCTGTAGACCCATAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGAC/AJTATATAAGATCCTCTTTTAAAAATATATTTTATATAAGCACAT GAAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAAC TAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTTATGATATCTTCTGTTAGACCCATAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAAAATATATTTTATATAAGCACAT GAAAATGGAATGAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTCTGGAGTTTATTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTGT[C/T]CACC ATTTCCATAACAAAAGAAAGCTACACAAAATTTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA/A/GTGTATTTAGATCCTCCCCCAG TGACAAAGTAACTGAAGTACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA/A/GTGTATTTAGATCCTCCCCCAG TGACAAAGTAACTGAAGTACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAACGCTGAACCTTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACACAATTTA GATGAAGTGAATTAAGNTAAATAAAATAAAAT[C/A]CAATTTCAAGAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCCAGCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCCCTTCCCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGTACTTAGGAACCAATCCACCAGAGAGACTCATCTATGTGA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTCC
S72904	51	G T ---	---	AGGATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAAAGTTCCTTT[G/T]AATTTGCAGTTTC ATTCTGGAAAATCTTTTGAGTTAAATAAGGATCTTAGGACGACACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAACACCAAGTGCTGAACCTTCTCCCTTTCTGTCAATTGGTTGCTTTAAATA TTGCAAAAGTCTGTGCTAAACAGTATTTGGAGTGTTTTTCAAGTGCTGTGA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAACCCATTAGATAAATGGCAGTACTTTAGACACACACAAACACAGAGAC/TJACACCTTTTGATATGTAAGTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCTTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTGGTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTCTTGTCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACCTTCTCACANGCTGTATTACCTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACCAGGAAGGCCCTGCCCCGCAGAGGCACATGNACAGGGCAGTGACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAACAGTTTCCCTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCCAGGCCCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCGGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAAACANGAGAAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCCTTAGCAAACNCTATGTTGTCAGGTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGCTCTCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	AGGACACAGCCTAAGGACATGAAGGTACAGAGTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTGTGGTACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCAATTTTAAATC AAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGIGATTTCTCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTTAGCAGCATTTCTGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGTNATCAGCGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAGNCATTAAAGCAGAAGTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACCTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCAATTTTTTTCTTTTAAATACAAATCTACTGGTGCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACAGINTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCAATTACA
ESTC156	32	---	---	---	GCAGCATTGTGACAGAGAGCGGCAAAACAAANCCCTGGCTGCCTGGGATGGAGCGGGGGGCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGGTGCAGTGGGGGCTGAGCTGGGNGCAGTCGGCAGTGTCAGTGGGCCGTTTG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTGCAAGTTGCTGTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATATTGGTTTGTAAACANCGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANITTTGCTGGATTAGAGGAAAGTGCCGCTCTGTTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCITTTATTCTATTAAAATACCTTTTAT TCTCTTTATTCCCATAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTTGCTCTCNTGTACAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTTAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCITGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAGCTTG ATTTTCACTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGATGGCTGG
ESTC188	25	---	---	---	---	TCTATTAAACAGGGTTATGTACACACCNTGTCAACCTCAAAACAGATGATACATCATCTTGCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAAATACCACITTTCCCTTAACCTTATCAGTCTAGTAGAGCTAGAGCNITTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTGCTGCCTCTCCCNCGCAAAGTCTCCCAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	---	TCTTACTTGGGTAGTTTAGCAACATTTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGGACAGACGCGNCGCGGCTGGTGGCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCAACTTTTGTAGAAATTTTGTGTGTAC AAGACACGTTGCA
ESTC208	43	---	---	---	---	TATAGCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	---	GGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGGCTTCAGAGCAGAGGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	---	CTCCAGAGTCCCTCCTCTCANACCAGGGGCGAGGGAGTTAGGGAAT
ESTC216	49	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	---	TTTTGTCAAGTAATGAGCAATACACTGANTGGAAATCTGCATGATTAATAACATTAAACAAGTTTCAAT AAACACACCCCA
ESTC219	32	---	---	---	---	GTACACATCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	---	---	---	TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTTCTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACANAAACACACACACACACACACACA
ESTC225	20	---	---	---	---	TGCACGTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	---	TTCTACTTTATTTTCATATTTCCACCACNATAACGACTCTCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	---	GCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCGCCAGAAATTAAGA
ESTC231	24	---	---	---	---	CAAAAGGGTAGTCATATTCCCCANCAACAGCATGATAAATAATTCAAC

[illegible]

DWU-252	94	A G ---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTACAAAGGCACTTTCATGTAAAGTGT CAGAAAGGAGCTACAAACCTACCTCA/GJTGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C T ---	---	GAACATTCCTCTGCAGCACTTCACTACCAATGAGCAATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCAATTATGTGGACTGAA/CJTCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTCTTTTGCAA CAAGACAAAGCAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAAA CTCGATGAATGTGTTGATTTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A G ---	---	GAAATGTTAATTGGGAGGTGAAAGGGTACAGATGTGCTGAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGGCACTGTAGAAAGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAGGTGAATGTTGAGGGCCCTTCACCTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCTTCA/GJGCACTATTTCCCTCTGTGC
DWU-1537b	89	A G ---	---	CTCTTAACITTCAGTTCCTCATCTATAAGAAATAAGGATTTCAGTTGTATCATACATAGCTCAGGTAATC CAGGACCAAGAAACCCAGGAGC/GJTGAGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCAATTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C T ---	---	CTCTTAACITTCAGTTCCTCATCTATAAGAAATAAGGATTTCAGTTGTATCA/CJTATAGCTCAGGTA ATCCAGGACCAAGAAACCCAGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCAATTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C G ---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG/CJGAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGCTTGTCTC
ESTD-ADAA	184	G A ---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTG/GJGCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGCTTGTCTC
ESTD-ANT1	160	T C ---	---	TCCTCTGTCAITTCCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAAACCAAGTAATCA TGGACTGCCCCAACTCGAAACAAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATGATCCTGT
EST10398 2b	168	A G ---	---	TGCCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCCAACCCAGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGATGTTTACATTTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTCTTCGGGCCAAAGAGGTATCTACCC/GJATAGTGTCTATTAGGCATTTG

EST10398 2a	147	CT	---			TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTTGATGATGTTACATTTGGGGCTTGACITTCACACCGGAGAAG CATTGTTTCTTTC/JTGGGCCAAGAAGGTATCTACCAATAGTGCTCTATTAGGCATTTG
ESTD-C7	14	GC	---			ATATCGTGGCCTTA/GCJTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90	TC	---			CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGCAATCACITTTCTTTT/CJCTTTTAGAGTACCGG
ESTD- GPPK2L	38	GA	---			AGTCTCATCTGGGGTGTCCAGGTAGATCCCTTTTACCQ/GA/JCCGAGAACTGCTCGATATC
ESTD- HRASb	82	AG	---			CTGGGCTGCCCCGACAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACCTCTATAGTGGGTGG TATTCGTCCACAA/A/GJTGCACTCTGGATCAGCT
ESTD- HRASa	37	CT	---			CTGGGCTGCCCCGACAGCTGCTGGCACCTGGACGGG/CJTGGGGCCAGGCTCACCTCTATAGTGGGG TCGTATTCTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81	AG	---			GGAGGCAGGAGTGGGGAGGGGGTCTGCTGCTCCAGGTCCACAGACAGAGAGCGGCCTCAGTG TATCCCCACCCCCA/GJTGGGCGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	AG	---			GTGACCTTCTCAGTTTAA/GJAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAACAGAAAGGAGGTATGTAACA
EST36751 7	36	CT	---			CCAACTGCTTCAATTTTAGCTTTGCAGGTTTAACT/CJTGATTACTTTTCTATTCAAAATCTCTGTA AAATTGAAATATGAACTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	109	AG	---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAAT/A/GJTTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCTCCTCTACCCCTA
EST18288 3	121	CT	---			GCCTCTATACCCCTGTGGTCCCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGAGAA GATTGACAGGTTCAATGCAGGCTGTGACAGGATGGAAGACTGGCTGCCCTGA/CJTGGGAGCCAGT GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAAAGGTAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31	CT	---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT/CJTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180	AG	---			AATCCAGCACCTTAGGAGGCTGAGGCAGGCATATCACAGAGGTAGGAGTTGAGACCAGTCTGA CCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGGG/A/GJAGGTTGTGGTGAGCCGA GATGGACCAATTGCATCCAGCCTGGGCAACAAGAGTAAACTCTGTCTTC

EST70523 3	182	G T ---	---	TTCCGCCAGCCOCCATCCTTGGCACCCCTGGTCCOCCCTAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGGCCGGCGCGCTCTTGGACACATAGCCTGGACCGTTCCGTATAGGAGG ACCGGTAGGCCCTTCTGTCCCGGCCCTTCCAGGGGCCAGCCCT[G]TACAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACAGT
ESTD- APOA2	101	C T ---	---	CCAGGTGTTGGCACGTGCCTGTATCCAGCTACTCGGGAGACTGAGGATGAGATCTTTTGAAC CGGGAGGGGAGGTTGCAGTGAGCTGACATGCTGCCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	C T ---	---	CAGTGTATCTGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC[C]TCTAGAGATACACAGAGC CGAATGTATCAATGGACATTCAGCAGGAATTCACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCIT
EST74167 6	137	C ---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGCGCGCAGCGCGGCTGGCGCGGACATGGAGGA CGTCCGCGCGCCCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCCGAGGAGC TGCGGTGCGCCTCGCTCCACCTGCGCAAGCTGCGTAAGCGCTCTC
EST43211 8	132	C ---	---	CGCTGTGTCAGTACCGCGGAGGTGAGGCCATGCTCGGCAGAGCACCGAGGAGCTGCGGGTGC CCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAAGGCC TGGCAGTGAACAGCGCGCGCGGAGGCGCGGAGGCGGCGGCTCAGCGCCATCGCGGAGCGCCTG GGCCCCCTGGTGAACAGGGCGCGCGGCGCGGCTG
ESTD- ARSB	126	A ---	---	GGAAGAAATGGAGCCTGTGGAGGAGGCGTCCGAGGGTGGGCTTTTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCACATCAGTGAA GGAAGCCCATCCCCCAGAAITGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144	C ---	---	TGTAGCCAAAGTCACCTGCATCATCTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGCTGGGCTGACCAAAATATACTGGGTTCTGTTCTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137	A ---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTCCGAAACCTGT CCATAAAGTAATTTTGTGAAGAAGGAGCAAGAGAACATCTCTGCAGCACTTCACCTACCAATGA GCATTAGCTACTTTTCAGAAITGAAGGAGAGAAAATGCATTATGTGGACTGAACCGGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTCTTTGCAACAAGACAAAGCAAGGCC
ESTD- BA511	29	A/G ---	---	GGGCAACATAGTGAACCCCATCTCTACA[A/G]AAAAACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGATGGTGCCACTGCA

ESTD- BCL2	116	A G ---	---	AGCTGGATTATAACTCCTCTTCTTCTGGGGGCGCTGGGTGGAGCTGGGGCGGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGCCACGCTGGGAGAAC/A/GGGGTACGACAACCGGG AGATAGTGATGAAGTACATCCATTAAAGCTGTCGAGAGGGGTACGAGTGGGATCGGGGAGATGT GGCGCGCGCGCCCCGGGGCGCGCCCGCAACCGGCATCTTCTCTCCCA
ESTD-BCR	69	C T ---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA GA/C/CAAAGAGGTCAGCTTCTGTTGTCCCGGAAAGGAGGCGAGGTGACAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCTGGCACA
ESTD- BRCA1aa	119	C T ---	---	AAGAAGAGAAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCAC/ATJGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTTAGGGGAAGGCAAAAACA GAACCAATAATAAT
ESTD- BRCA1bb	139	A G ---	---	ACTAAATGTAAGAAAAATCTGTAGAGGAAACCTTTGAGGAACATTTCAATGTCACTGAAAGAGAA ATGGGAAATGAGAAACATCCAAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAATGTT TTTAAAG/A/GIAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAATGAAA
ESTD- BRCA1cc	126	A G ---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGTATGACCTGTTAGATGATGGTGAAATAAAGGAAGATAC TAGTTTTGCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAGCGTCCAG/A/GIAGGA GAGCTTAGCAGGAGTCTAGCCCTTACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST51212 0	122	A C ---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTCTCCACAAGCCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACA/A/C/JAAAGGCCCT CTCTACATCT
ESTD-C1R	40	A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTT/AG/JATTTGCTCCGGGAAGCACATTCAT CAA
ESTD-C1R	40	A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTT/AG/JATTTGCTCCGGGAAGCACATTCAT CAA
ESTD-C6	31	A C ---	---	CCCAGTCAGTTTGGGGACAGCCATGCACTG/A/CJGCCTCTGGTAGCCTTTCAACCATGCATTCCTCATC TAAGCTCTGCAAAAT
EST20118 2	119	C ---	---	GTCCGAATCCTCCTCTGAAAGTGGCCGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCCCTTGAAGCTGGAGTGGGGTTTAGGGACGCGGCTCTGCGTGCATCCTAAGCTCT GAGAGCAAAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	67	A G ---	---	ACAATCCAGGTACACATTCAGAAAGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA /A/GIAGGATTCAGGAAGGAGGCCACGAGGATCGAAAGTTAGTGAAGTC

ESTD- CB22	119 C T ---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGGAGATGCCAACCCATAGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCCCTTTCCGGCCCTCTCTCTCACACAC
ESTD- CB23	136 C ---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCCTTTCCGGCCCTCTCTCACACATACACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCAATTACCTCTTCCCTTTCCAGAGGACCTGAAAACGTTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145 A ---	---	ACCAAGCAGACAGCTCTCAGAGCAACCTAGCCCAATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTGGCTGTGTTTGAACCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGAACACGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACAGACAGACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	GTTTTCTTCAGACTGTGGCTTCACTCCGTAAGTGAGTCTCTCTTTTCTCTCTATCTTCGCCGTC TCTGCTCTCGAACCAAGGCATGGAGATCCACGGACACAGGGGGTGGAGGCCAGAGCCACCTG TGCACAGGTAGTCTACATGCTCTGTTCTGTCAACAGAGCTTACCAGCAAGGGTCTCTGCTGCC ACCATCCTCTATGAGATCTTGCTAGGAAGGCCACCTTGATGCCGIG
ESTD- CB27	125 C T ---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGCCCTGGTTGCATTTTCAGGAGTGTCTGTGGAGTTCTGCTCATCTACGAC[C/T]TATCTTC TGATTTAGGGAAGCAGCATCCCTTGGACATCTGAAGTACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTCTGTTTCATCTGATGGAAGTCTCAAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/TATGTA TTTCTTAAACAATAAATGAAAGTCCAAAATTTACTCTTGATCCATGGACTGCAGAAATAAATGTTA TTTTAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATTTTGAAGGAACTCTGTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G ---	---	CAGGCCAGGTGGTGGTGAGTCCATCCCGGCAGAGAACAGGTGAGCCACCACCTATGCjA/GjCA GGTTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	AAAAAACATTTTAAACCTTTTCAATCATATACACCATA/CjA/TTCATTTTCCATATTAAGTCA GTTTGAGCTGAGTTTCCAAATTTCTGCAATCTAAATGTCACTAATTAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	CATCCCAAGCCCATCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGCCCTTACCTTTGTAGTCCATGGGAAAGGCTCTCTGCGGGGGTG GGTTGTGTGGCTATGTGGTGTCTGTGTAGAG[C/T]GGGGGCTTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTTGTCTTCCACCTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ---	---	CATCCCAAGCCATCCTTAGCCACTGGCAATTTTGGCGCTCTGACAGATACACTCAGGCGCGT CATGCTGCTACACATCCAGGGCGCCCTACCCCTTGTAGTCCATGGAAAGGCTCCTCTGGGCGG GTGGGTTGTGGCTATGTGGTCTTGTGTAGACGGGCTTTGGTTTCAGTTGCACATATTGCGT ATTGCAGATTGCTTTGCTTTCCACTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGGAGGAGAAATGCTTGAACCCJA JGJGAGGCGAGAGCTTGAGTGAGCCAAAGATCACACCACCTGCACCTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAAAAATCCAAATAAAGTACACTGTAAATAAGAAATTTAACAGAATATCATTTGT TTATTCAAACTATTTATCACTATTTTATTTGTAAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGGTATGTTTCCJAGJGGAGCCTTGATGTCACTCTGTATCTCCT CAGGTATCCCACTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGCTTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTTATCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTACTGGATGTTCTGTTCCGCTTTCACGATGG CAGGTATGAAATATAATACTGTCTCTTTATTTGGAAGGATGCJCTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGCTTTATTCAAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTTATCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTACTGGATGTTCTGTTCCGCTTTCACGATGG CAGGTATGAAATATAATACTGTCTCTTTATTTGGAAGGATGCCGGTATGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGJGTCTCTCTACATCATCTCTTTCACAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTJAVJCTGTGGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAG ACCTCTGATTGTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCAJC GJTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGAGA CAGAATGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCTGATTGTAGGAAGGGAGCAGCAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T ---		TCCCAGCCCTATCGGTCAATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAAACGGTCAGCACCCCAACTGAACTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TTJCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---		TCTGCCTTTGGTCAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGAGCCCGGTACAGCCCCATCCACCCAGCCACCAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCAGACACTCCCGACAGCCCCGCCAAACCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---		AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGCCATAGTAGGATGTGGCGGGCCCTGGCTGG CACTGTGGAGTTCTCTGCCACACAGGTGATTCAGGTGGC/TTACTCAGCTGGCTCAGAGATGCC ATAGCCACAGGAGGAGGTGCGTATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---		TCTTCAGGATCCGCATCTCGCCCTGGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGGTGGGTGAGTGC/TTJGGGGCCGGTGCAGACCCACCGGGCTGGAGGACTTCA CCCGCTCACCTCCGTTTCTCGACGAGTCTCCGCATCGTGTACT
ESTD- ETS2	43 A G ---		ACTCACAGTGCTTTTAAGTGAATGGTCGAGAAAGAGGCAC/AGJGGAAGCCGCTCTGGCGCCTG GCAGTCGGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCAAAAGCGGAGCATGCTGTGGACACA CACAGACTATTTTAGATTTCTTTTGGCTTTTGCAACCAGGAACAGCAATGCAAAAACCTCTTTTGAG AGGGTAGGGGTGGGAAGGAACAACCATGTCAATTCAGAAGTAGTTTG
ESTD-F9	111 A G ---		AGATCCTGATGATTTTTCTATTTTTCTAAATGTTTTACAGTTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTGTAAGTATGATGTTTAA/GJGTCAAACCTCATTTTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---		CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGCAGCTCATGACAAATTTGAAGCTGACAATACACAAGGAAGGAATAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTGGGTGTCACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GODH	200 C G ---		CGCAGACCGGTGAGTGGGGTCCGGAGTGTGGAGGGAAGGAGGGAACCTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGAAGGGACCTCTGGTCGACCGGTGTTCTGCTGCCCTGTTACGCTGTCTGTCTGCCCGCAGT/CT GJGACTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	88 A G ---		GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA/AGJACAGTAGAAGCCCTGGCAGGAGAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGGGGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTGC ACCTGCAGCCCTAATTACTCAAAAGCTGTCCCGAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCACAAAGAGACCGGCTC[A/T] AGGATCCCAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCAC[A/G]GGCATCA TTGAACCAGGTTTCCGTCAAAGACTTGAATTTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154 G ---	---	GGCTAAATTTCCGAGCAACTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGACAGTTTGCAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTGCTTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTTCAAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACACAAGCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTCTCTCTTTCATCTTATAGATTGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATAATTCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTCTCTTCCCTTGGA CTTTGAGTCAAAATGGCTGGACTTGAGTCCCTGAACCAAGAAAGAGAAAGAG[A/G]CCCCAGA AATCAGGTGGCACGTCGCTACCGCCATCTCCCTCTCACGGGAATTTTCAAGGTAACCT ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGTG[C/T]CTGGGAGAAGAAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCATGTTGTGAGTGACGGGCGAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATTATTATTATTATTTATTTTATTTTG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCCTCTGGGTTTCATGCCATTCTCTGCTCAGCCTCCGAGTAGTGGAATACAGGCACCCGCC ACTGTTCCCGGCTAAATTTTGTATTTTGTAGTACGAGGAGTTCACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTGGGTGCTGTTCTCTGCCCTC[A/G]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGTGGCTGGACCCAGGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTGGGCTGCTGAAGCATG TGGGGGTGAGCCAGGGGCCCAAGGCAGGGCAGCTGGCCCTTACGCTGCTCAGCCCTGCTGTCTA/ TCCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGGCTGCTGCCCTGCTGGCGCTGTCTGGCC CTCTGGGGACCTGACCCAGCCGACGCCCTTTGTGAACCAACACCTGTGGC

EST45311 0	151 C T ---				GCCTCTCTCTCCAAATCTGTCCCTATAGTTTTCCCTATTAAAGTGAACATACATGCAATCTTTTAGT GGATAGTGCACACAAACACACAGCCATTATGGGAAGGATCCACGCTGTGGCCATATTGTAACA CATTTTCTGCAAATC/TJACCTCTTTCAITTAACAGCCCTATTCAATGGCCCTTTTCTTTTCAGTA GTACATACACATCTGTGTCATTGTGTAAT
EST65258 8	80 A G ---				TGCCCATCAGCGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCAACCAATTAACACAGAAAT CCAGTTATTTTCG/TJGJCCCTCAAATGACAGCCATGGCGCGGGTGTCTGTGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---				ATGCAGGATGAAGGTGGACAGGGAGG/TJGAGGGCCAACTGTCTCCAGGCGCTGCAGATGTGG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T ---					ATACTAGTACAAGTGGTAAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTAAATGACAGTGGAAG TTTTTTTTCTCTG/TJAAAGTGCCAGTATCCAGAGTTTGGTTTTTGAACATGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTCTGTCTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATTAATCTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCT/TJGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACAGTATTGATA
ESTD- KRT10a	133 A G ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATTAATCTCTAAG GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATAAGTTATAACAGTATTGATA
ESTD- KRT8b	231 C T ---				ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---				ACCCTCACCCCTCCCTTAGCC/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATATA GGCTGCCTATCTCTCCCGTCTCAGGTTTACCAOGTCAACATTGACACA
EST75099 6	82 C T ---				CACCTGTGTGTCTAGATCTCCTCAGTGGCGGCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/TJGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCACC CCTCTCCTTGGCCGCTCTTGAGGTGTGG

ESTD- LF79	142 A G ---	---	GGTGATTTGAGGCTCAGTTAATTTCAAATTTGTAACCGTAGCAAAACTGCATTGGTATTAGA AAAATAAAATTTCCAATATGATGTCTGTATTACCTGCCTCTGCCATGCAGCATATAGCCTGT GGAACTTGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTAGTTATTAGGCATGGTTACCTGTGATTTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCTGACACGTGTGACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA
ESTD- LMP2	35 C G ---	---	A TACACACTTTCTTACCAATTCACCTGAAAACGACT[C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGCCCTGCTGCTGCCTGCA AGGTTTGTCTTAATTCATTCATGCTCTTCTCATCTTTTAG[C/T]AGCTGTGGGTTTGTGTTG TTCTCTGTTTGTCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAAATAG AGATTGTATCAGAAGTTCAACAACATTTTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTCTGATGCTGCCTCCCAAGCTCTGTCCCTAG[C/T]GAACTTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTTGGTCTAAGTTGCTGATTACC[C/T]GGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCTCTTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAAC[T/G]TACCAGATCCACAGACTGATATGGCTGGT AACATGGACTTGTATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCTTAA/GGCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCAITGAAATCT GAGAAAACTCTTTTAAACCTCACCTTTTGTGGGTTTGTGGAGAGGTTATCA
ESTD- NFB1	107 A G ---	---	TGTCCTAGGCCCCAGCCCTGCTTGCTCCCTGGCTGTTATCTTC[A/G]GTACTGCAAGAGAACACA GACAT
ESTD- NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCGAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGTGATATTGGATCTTTTGTGTGATTATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG[C C/T]ATTCCCTGTGTTTAAATAAAAT
ESTD- NRAS	202 C T ---	---	GCCACCAACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGG[A/G]GTACGCCGTGTATCATCGGAGCGGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTTAGACAGACAAAAAC
ESTD-PAI1	100 A G ---	---	TAGACAATCAGTGGCTGGCT

ESTD-PAR	120 A	---	CTCTTCAGGAACCAACAGTCTTCTTACCAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA
ESTD- Per/RDS	74 A	G---	ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT
EST68308	29 C	T---	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTCTTCTTCACTTTTCTGTGTTCTAGAACGTTTCTTAG
5			GACTGGCAGTTTAAAGCTTTCACTTAGGCTTCTGTATACCCATGCCC
EST54045	39 A	G---	ACCTACAGACGCTCGCTGGATGGTGTGCCAACCCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG
6			CTGGAGA[A/G]GAGCGTCCGGAGACCTGGAAGGCCT
			GGAAAGAGATTAAAGAGCTTGATTGGA[C/T]JAATTCCTGTTCTTTGAGTGTGGAAGAGTTTCATGTCT
			TCTGCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
			GGAGAAGTAGACTTTAAAGGTAAAGTAAGTAGTATTATTTTA
			GGAATATTAAAAATATTTTAAATACCTCCATTTTCTT[G/C]TCTTTTGTAGTGAAGATGATACCTGCG
			AAAAGACATGGCTAAAGTTATGATTGTCTATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
			TCTGTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTGACTTTATCAT
ESTD- PXMP1	88 A	G---	ATGAAACATGGTCTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAAGGGCTCTCTTTTTTTTA
			ATGCAGAAAGAGGGGAAAAA[A/G]GAGCGAGCTGTGGTGACAAGGTGTTTTCTCAAGGCTCATAC
			AGATTCTGAAAATCATGGTCCCTAGAACAATTTGTAAAGAGGTAAGTCTTATGAAAATTATAATCTT
			CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAAGAGCGTGC CGGAGACCTTGGAAAGG
			CCTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCCGAGGGCGCAGACGACGAGG
			CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAAATAGTGCACCT
ESTD-RDS	127 A	---	CCAAGAAACGTGGATCTCCCTCATCCAACCTCCGAAAAGTCTGAA
ESTD- s14544	94 G	T---	TTGGGAAGTTAGAGCCTATATTAATACGGAATACGGAATTAAGGCAGGACACAGAGGCTTAATTGAAAAA
EST52908	45 A	C---	TATCCCAAAGTTGAAATGCTCAGTT[C/G/T]CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTTA
0			ACCTCT
			ATCACAGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG[A/C]TGGTGGTCTGCAAGCCCTT
			TGGCAATGTGAGATTGATG
			AGGAGAAAGCTGAGGAGGGGAAGAGAGACAAGAAATGACATTGATGATGAAGATGT[C/T]GGGCTCAG
EST19590	55 C	T---	GATGCCGGAAAATGAC
			TGAAGCTTCTGCCACGCTTGCAATGTTTCTTAGGAGAAC[C/T]GGGTCATACCTTTATCTATAGCCTT
EST76136	39 C	T---	CCCTAGGTCTT
			TGAAACACCTGTGGTCCGGAGCCAGGTGTGTTTCTCTCTGGAGCCCTGAGGAGTTTGTTGCTGTGTG
			CAGTCCCCCGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCCGGAGAAGAC
ESTD- SPTB	176 C	T---	ATTATCCACCTGGCCATGTCCCTGGCCTGTGTGTCAC[A/C]TCTCTGTGAAGACACCCCAACCCCTGCG
			CTCCCCACCCAAAGCCAGTTTCTTAGCAAGGGCAGGAC

ESTD-TAT	224 C ---			AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTCCTCTCACCTAGAACGTTTGTTCACACTTTCTCCAGTATGGATGGGATTTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACATCA
ESTD- THRb	125 A C ---			TGGGCCCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTTGATTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCATGAGGCCAGTCTCAATCACACAGGATC[A/C]CTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCA[G/T]ATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTCATTTGGCCATAGTCCCTATGGGATGACA
ESTD-TYR	122 G T ---			AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACTTTTATACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACCT
ESTD- TYRP1	222 A C ---			AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACTTTTATACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACCT
ESTD- VB12	148 C T ---			TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---			TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---			TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCAACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607	105 A G ---			CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCAC[A/G]TGGCGGGATGGCGGGGAGTTC TGGTTGGCGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGAGGGGGGGTCCATGCTGAGATGTAGATGCGGOC
ESTD-VWF	36 G ---			AGGTAGGAAAGCAAAGAGTTGATTAGTGAAGGAGAGATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
EST71770	189 C G ---			AGCACCACTCTCACGTCAAGCCTCAGCACCCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCACAGAGAGTTATTTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACCTGCAGAGTACCAG[C/G]TGTGGTGGGA AGGAGTCCCAGTCCCAGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
ESTD-TNFAb	152 A G ---			TTCTGCATCTCTGTCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAGACCCCTC[A/G]GAATCGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATG CTTGTTGTCCTCACTTCCAAATCCCGCCCCCGGATGG
ESTD-TNFAa	88 A ---			TTCTGCATCTCTGTCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAGACCCCTCAGAATCGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCTCACTTCCAAATCCCGCCCCCGGATGG
EST52418	113 A G ---			CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCCCAGTACACCTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGGAGTACGGGCTGCAGGCATACACT[A/G]AAGTGAAAACTGTGAGTG TGG
EST13586	89 A G ---			CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCACATTTGCCAGGA CCAGTGAGCAGCAACAGGGCC[A/G]GGGCTGGCTTATCAGCCTCCCAGCCCAGACCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976	123 A T ---			AGGCAGAAACTGGGCCCCATGCGGGGGACGTGAAGGCCACTTGAGCTTCTCGGAGAAGGACCTGA GGGACAAGGTCAACTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[A/T]CTCTCTC CCTCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGCAGCAGCAGCAGCAGGAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458	140 A G ---			CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTCTCCAGTGTCTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGACGACGGACCTGTCCCAAGCCAGATGATTACCATTTCCACAGTGGT CCC[A/G]TTAAAACATTCTATGAGCCAGGAGAAGATTACGTATTCCTGCAAGCCGGGCTATGTG TCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60	C T	---			AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCCCAGCCTAGCA CTGGTGCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAAGAGACAGATATTAGAGCTGGGGAATGTGG
EST39852 8	106	C G	---			CGGTCTCTCCAGGTATTGTCAGAAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTACGJGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAGGCCCTGTTCCAGTGTAAAGGATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112	A G	---			ACCTGGTGTGCTGTGGGTGAACCTGGTCTCTTGGCATTGCCGCCCTCCTGGGGCCCCGTGG TCCTCCTGGTGTGGGTAGTCTGGAGTCAACGGTGTCTCTTACGJGGTGAAGCTGGTGTGATGGCA ACCTGGGAACGATGTCCCCAGGTCCGATGGTCAACCCGACACAAAGGAGAGCGGGTTACCC TGGCAATAT
EST36027 2	120	A C	---			AGTGACTTCCAAGGAAATGGCTACCCAACTTGGCTTCATGCGCCTGCTGGCCAACTATGCCCTCAGA ACATCACCTACCACCTGCAAGAACAGCATTGCAATACATGGATGAGGAGACTGGJACJACCTGAAAA AGGCTGTCAATCTACAGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGATGGTGTCTCTAAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112	A G	---			AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTCTGCTACCTTTCAGJGGGTGTTCAAGGTGAAAA GGTGAACAGGGTCCCGCTGCTCCAGGCTCCAGGTAAGTCACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97	C T	---			TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACA/CJTJTGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACTTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150	A G	---			GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGTGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCTCATCATGAAAC TGGAGGCCCGGCATJGJGTGCTCATGCCTGTAAATCCAGCATTTTGAGAGGCTGAGGCGGTGGAT CACTTGAGGTGAGGAGTTTGAACCAACCTGGCCAACAT
EST12274 0	135	A G	---			CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGTCTCCAATAGAGCCTTACCAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCTCTCATGACCAATATCTTTCCCTCCTTAGGATGAGGTG A/GJTAGTAAATGACCGATGGGTGAGAACTGTTCTGTCAACCATGGAGGATACTATACTGTGAAGA TAAATTCAGCCACAGAGCTTGCCAGATC
EST76807	91	G	---			ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATGTCTCTATCTCAGCGGCCCTGTCTC CAGTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCAGTGCCTCCT GCTGCCATGTGGAGTGGTCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	---	TTCACTTTGTGGATTGTTCTTTTGTCTGTGCAGCACCTTTTCAACATGATGTGATGCCATTTGTCCAAG TTTGCTTTGGCTGCCTGTGCTTTGTGGGATATTTGAAAGAGATCTTTTGCCAGTCCCAATGTCTCTAGA GAGTTTCCCAATGTTTCTTGTGTAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTGATTTCTGTA
ESTD-RYR1	109 A G ---	---	---	CTTCGTACGGGAGGTACGCTCCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGACACGCGAGACTTGTCTACTATGAGTGGGGAGCTGTGTGCACTCATGCCC CGCTCCTCTGGAGCTGAGCCACTGAGATCAGCTGGAGTGGAGCCACCTGCCCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGCGAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTACTCTCTGCTGCCTGCAGGATGTG CGTGGTGGAGTAGCCCGACTCTTGACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2	100 C ---	---	---	GATAAGTACACTGAGGCCCCAGGAGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGCCCGTAGGGAACTGGGGGATCTAGGGATGGGTAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGAGGCCGTGGAGGAGACAGGAGATGGGC TGGATGAG
EST4438 7	62 C T ---	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGA/C/TG TCCTGCTCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
ESTD-PBDA	103 A G ---	---	---	CCTTCATGCCCAGATGGAAATCCAGTCCCTTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/GTCTCTACCCGACGCTTGCTCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
EST12839 3	122 A G ---	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGT/GTCAAGTCCA AGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACCTTAG
ESTD-CTLA-4	48 A G ---	---	---	ATGGCTTGCCTTGGATTTCAGCGGCACAAAGGCTCAGCTGAACCTGGCT/GJCCAGGACCTGGCCCTG CACTCTCTGTTTTTCTCTCTTCTATCCCTGTCTCTGCAAGAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD-ACE	96 C T ---	---	---	GATCAAGCAGTGCACACGGGTACAGTGGACAGCTCTCCACAGTGCACCATGAGATGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TGTCTCCCTGCGTCGGGGGCCAACCCCGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACTCTGCACAAAATCGGCCCTGC
EST54419 8	88 A G ---	---	---	CTTCTGCCTAATTTGAATGATATTGCTGTGGAGCTGAGCAGCTTTTATGGCAAAATGATCACTA TTTTCTTGACCCCTACTTAC/GATCTCTGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGTCTA CTATAGTCCAAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGAGTAAACCTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAACCATAGCCTAGJTTCGTAGCCATATTAATGGTTGTGCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATGCCAGCTCTTCCAATCTCCATCAOCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGGAGGGCCCTAGCCGGGCCCCCTGCTGGGCTGGCGGTGCTGGCCACC GTGGGAGGCAACCTGCTGGTCATCGTGGCCATGCC(C)TGGACTCCGAGACTCCAGACCATGACCAA CGTGTTCGTGACTTCGCTGGCCCGCAGCCGACCTGGTGATGGGACTCCTGGTGGTGGCCGCCGGGCCA CCTGGGCGC
WI-567b	48 A G ---	---	TCTCACACTGACCCCTACCTTCATCCTCACCTCTGCTGCCCTGGTTCTGAGGCCCTCATCTCTTTTA CAGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGCTCTTCTTCCAATCCATCTTCAAAAG GCTGCCACTGTGATCTTCCAAAGGTGATCTGATGCTACCACATCTTGCTTCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCCTTCTGTJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGACGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACAGAGATTAA CATTTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCCTTCTGTJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGACGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACAGAGATTAA CATTTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTATTACATTAGTCTCATATTCTGAAATATTAT TTTTTACA/JGJTACCCCTTTGATTTTGTATTTGTAACGAGAGATTACAATACAGTAACGC TGTTCAATTGATAGTGTATCAAAATGCTAAATACCTTTGGGTCAACATCAAAATAGAAAGAAA CTTACAAAGTTTATTGCTTTATGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA(C)TTCCTTAAGTGTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCGAGGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATGAGGTAAACCTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGACCCAGCCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG(C)GJAGCAGAAAGCAGCAAAAGGAGAAAGGAAGT

WI-2625	98	G A ---				GGCAGCTCTGGCTGTAGTGGTAGACAGCAGCTGAAGGATGGAGGAAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAGGCTTATTAGGA[G/A]CAAAATTGATGATACTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAG
WI-2924	54	G A TAGG	TGACCTTCCTA GTCCTCTCTTA		GCCTAAGTGT AATCACAGGG	TCGTGTGCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTTTATAGG[G/A]ACCCTGTGATT ACACTTAGGGCTACCTGGATTATTTAGAACAATC
WI-2939	72	G T GTGCCITT	GGCTTGTCTCA		CTTGTGAGGG AAGTCTTG	CCATTGTGAGTTGGGTGGGTCACTTTGTCACTCCCTGCAGCTCAACAAAGTGGCTGTCTCAGTGC CTTTG/TJCAAGACCTTCCCTCAACAAGAAATGTCTTTCCATGCTCCCGTGTCTTTGAAAATTCGACT TTATCTGAAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99	G A AGACGAG	GGTTATGCCGC		TCAAGTATTGC CTTGTGIGG	CTTGCTACCATGCATTTACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTTATAAAACAT CTTGCCATCGAAGGGTTATGCCGCAGACGAG[G/A]CCACACAGGCAATACTTGAAGTGACTTGGA GAATAAAGATTTGGATGGATGAAGCAGAGAGAGATGCTAAAAGTGA
WI-3473	101	A G GCOCTAGGGA	AAGCATTTTA		CCTGATGTCAC CAACATTTCT	GGAAAAAGAACCTGAAGGATGAGTAGAAGTTAATTTGGGAGATAGTTGGTATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAGCATTTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCGAGCGCTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTGCTTGGCTCCOC
WI-1796b	29	A G ---			---	ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCGAGCGCTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTGCTTGGCTCCOC
WI-1796	29	A G ---			---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGGTGAGT AGTCACATTAGGTATTTTCCAAATAA[C/T]AAAAATGCCCTCTGAAAAATATCTCTCCCATGTCCCTGTCT TAAATATAACATTTTCCC
WI-4360	93	C T AAATAA	GTAGTCACATT AGGTATTTTCC		GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTTGGCAGAGCCAGGACAAATTCAGCTGCCGATTTTAAATAGATTCTGCAGCAGCTGCAA CAGGAACCAAAATCAGT[C/T]GGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87	C T ---			---	GTTGTGCCCTGTAGCAGACACAGAAGGCA[G/G]AGAGGAAAAAGCCTTTTGTCCAGGGGCTTACAC TGAATCCCTCAAAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28	A G ---			---	CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACCTAATCCCCCATATACCA AGGGACAAATGTATCTGTTTCTACAAATATACAGTAGGAGACATATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTTAAATTGAGTGAAATACCAATAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTACTAGGTGCCTATAAATAGC
WI-1980b	140	C T ---			---	

WI-2015b	190	A G ---				TGTCAGATAGTCGGTCTCTACCTAGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCCAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACTTAVGJCATATACTT CTAATACCATAGAG
WI-754b	49	C T ---				GAAGGCACAGGGAGAGATGGCTGTCTATCTACCAGCCAGGAGAGAGC/CTACATTTATTGGTAA TCCTATAAAGTGCACTCTTAAATTTGTATTTACTTTAGA
WI-754	22	T C ---				GAAGGCACAGGGAGAGATGGCTGTCTATCTACCAGCCAGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCACTCTTAAATTTGTATTTACTTTAGA
WIR-1b	56	A G ---				AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGATGATCGTACATCCAVGJTGCGCTG GAGGGTGATGCCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56	A G ---				AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGATGATCGTACATCCAVGJTGCGCTG GAGGGTGATGCCTCTGAGGACATGGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72	A G ---				TAAATTTAAATGGGGCCAAATACACAGTACTTATCTACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGTAVGJCTAAAGTTATTAGCTCAGAGCCCTCACACATTTCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T ---				TAAATTTAAATGGGGCCAAATACACAGTACTTATCTACAGCATTTCTCTAAAGGCTAAATAAGAA GAATGATCTAAAGTTATTAGCTCAGAGCCCTCACACATTTCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47	T ---				GAGCCTTTCTAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209	C ---				CGGGACAGAGACAGACAGAGAGAGTTCGACGATTCACAAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196	C ---				CGGGACAGAGACAGACAGAGAGAGTTCGACGATTCACAAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194	C ---				CGGGACAGAGACAGACAGAGAGAGTTCGACGATTCACAAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5a	37 A	G	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTTAGG AGGTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACAC AGTTTACGTCAG
WIR-6	63 A	C	---	TAACCTGAAACTTTGTCTTCCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGAOCCAGAA[A/C] CGCAGTCTGGGGTTGGGGCAG
WIR-7	12 C	T	---	TTCTGACTATT[C/T]AAGCATCTGTAGAATAATTGAATACATAGTCTTGAGATTGATC GGCGTCTATGACTATCTGGTCAATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46 C	T	---	AAACAGAAAAATAGAGGTTAAGGATGGAACATAAAAGTTGTCAGAAGAGGTATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAA
WIR-2	56 C	G	---	TGCTCTGCTTATGCCTGCCTCTTCGCTTGGCAGGATGCTGTCATTAGTATTTACAAGAAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGCATGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93 A	A	---	GGTCATTTCCTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTGTTCTGTCATCTCTCCC CCACATACCAACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATAGGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	
WI-18612	37 A	G	TGC	CCTATATTCA AGTTTGGAAA TTGATTGCTG CTTGCAAT CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTCAATGAAGAATGCATAATCTCTGAAAAATTATGAAAAACATCCCT

WI-18517	87	C T	CAGGAATCAG CAGCTGA	TGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGAGCCTGA/C/T/GTTGCACCTGTCCAAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAAA CTGCACCTTTT CC	CGATTGACAAACCTTTTATTTTCAACTTAGGTAAACAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA/C/T/AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	GCTGTCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAA/T/C/GCTCCGTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGTTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCAAGGCTGTACCCAGGCTTCTGTGCGAGCACACACCAAGGGCAGGTGGGCTTGAGGAGGCC CTTGAGGAACACAGGCTTCTCCGAGGGGTAC/C/C/CAGCAGGGCCTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGGCAAAACCTTGTTTAATTGCAAAAC/C/G/ACTTAAATTTACAGCACATTCATAATGAACCAAC AGGAGAGTGTGCTGACTTGTACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTOGTGGGTG GGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATCCTATTAGGATATGAAAGGATTGAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGTCTGGGGTGGGGGTGAGAGT/C/G/GTCCCTCTC AGTGGTATTGGGAGC
WI-18533b	91	T C	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTAACTCCCGAGATTTCCTCTTTATTT TATATTTTCAATTTTTCATCCTAA/T/C/TTACTGAAGCCATTTCTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTAACTCCCGAGATTTCCTT/G/CTTTA TTTTATATTTTCAATTTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTTCAGAT TTC	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCACTGATA CCTTGTTTCAGATTTC/C/AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTTAGGGGGTCTTTTCAATTTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/T/GCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGTT CT
EST10030	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACACTGCTCAGCAGATGACTTAAAAATTT CCCTTAGCCATTTTGTCTCTCAAGTCCC/T/C/TCATCCATACCACTGCTGATTG
EST10052	24	G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/G/A/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCATAACCTGGTGGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

EST10605 2	118 C G ---			---	CTTGGTAAATCACAGTCTCTGTTATCATACAAAAACTTTGTCTCTGACAAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGTTC/GTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G TAATCT	CTCTCAAGTAG ATAAGAGCA	AGAAAGAATT TTGTTT	---	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAATCTTTCTGAAAATTTAGCTTATGAACCTCAITACACTGCAACCAGAGAGGAGCAC
EST11260 8	101 G T ---			---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---			---	TTTGATGGAGAAATCCGAGGCCTGCCAGCATCCCCACCAGTAGATTTCTTTGGACGAAGAAAAATCCT TCTGTGATTACGCTTTACCGCTTTCCCTCATCTGCTGGTGTTC/JTTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G TGGAGCOCT	CCAACCTACTT T	CTAAAAACTCC T	---	GAATTCCTGGTATTAAATAGCGGGTGCCACAGGACACATAGGAAGAGCATCCAACTACTTTGGAG CCCTA/GJAGGAGTTTATAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G ---			---	CCAGGAATAAAAGAAAAAGAAAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA/GJGACTATTTCACTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---			---	CTTGCCATTTATTTTGTCATGTTGTTCTTAAAGGCTGTGAAAGATAAATTGGAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAAAAGTAGCCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG	---	AGAGCAATGGTGGCGATCTCAATAAGCAGCTCATTTTGATTAC/GA/GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCCTCCACAGAACTTTCATGCCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G CAAAGTCTGT	TTGTATAATA ACACTCAGTA	GGCTGGTCACT TCCTGGAT	---	GCCTAGTAATTCAAAAGGAACATGTTGTATAATAACACTCAGTACAAAGTCTGT/GJATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCAITTCATAGTTTTTGAATC
EST12055 9	32 T C ---			---	GTGGAAAATTTTTTATCTGTACGCTTTCC/JG/JATTATATTATCTTGTCCTTGATTTCAGCACCC CACCCGATTGCGGCAGTGTCTTCTAAACTGTGCCCTGTGAGCTGTAAAAAGTCTTCT
EST12492 1b	95 A G ---			---	CCCCTAGCAATGACTTGGAGTTGTGCCAATTACCAAGTTACATACTGTGGCCAAAATTAAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT/GJGGAAACGCACAGCAAAATTGACGATGCAGCTTTTA CCTTTTTA
EST12492 4	25 A G ---			---	ATCTTGAGGTTTCTGGGCCTGTGAG/GA/GAAGTGACATCTTTTACTTACCACAGGTGAGGAACCCAT AAAGAAACTGTAGAAAAGATATCAGGTGAGACTTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAACCAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAGTGGGTTTCGATGAAGAGAAAATGCTACGGGGAAATGACCATTTTTAAGGGCCATGTG GTCTGAGGCGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAAATGTATCGGTAAAAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATTATCCAAATGACAGTGTGCTGAGAT[C/G]ATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTCATTTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCCGGC[A /G]TTGAGAAATACAATATTGAAGAAGAGTCACTGCCTGCCCTCTGGAAAAATCAGAGTATTTGA
EST12817 9a	22 C A ---			TTGGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTGCATGAGGTTCTCATOCATGCTCCACGG GTTCTGGGAGTGACCGGGATGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCAITGCG
EST12941 8	23 T A ---			TCTCAGCTCCACCTGACCTGCAT[A]CAACAGCCCAAGTATTTTACCAGAAATTTGTTTGGGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACCTTGTTTIG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTTGCCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTTCTTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAAATGAAGCATATAAACAGTTAAAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCAC[A/C]TGGAGCAGAAGCAGCTTCCCACCCAAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAAAATGCAC[A /G]TATTTAAAGTTTACAAATTTGAGAAGCTGACACGTTGCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTTAAAGATTCTCATAGCTGCTTAGGTTTGTCTTCC[C/G]TJAGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTTCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAAATAGTCT GGCCATT[G/G]GACTAACCAAGTTCTACAAATTTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAACAACAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGGGCTTTTACTGAACTTACAACCAACTTGGCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACAGAGGGTT TGACAAAAGA	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAAAACACTCCCATCAGTAGCAATACAAAGTTTATACATTTTAAACCAGATTTTCTCAGG CCTT[C]TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCCCTCTTGTATATAACCA

EST13278 2a	51 A G G	CITTCACCGAA CAATATTTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAACTCCAAACCTTTACCGAACAAATATTTTAGG[A/G]ATTTGAAATAT TTCTGTAGTTCTCACCACCCCAAGATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTCT AGTCCAAGA	GATGGAATAAT TGAGGAAGGT	GCTCACTAGATGAGCATTGACCAAAATATTTAGATAATACCTGTTGGGAAAGTGTGAATTAAGCC TGCCTGAGAAATCCACACATTTGAGTCCAAGA[A/T]AACCTTCTCTCAAAATTTTCCATCTCCCATCAGA G3
EST13290 9		CAATTTTTAGA AGTTGGGTT	AAATCAGTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTCTT[A/G]CTGAAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCATATTTTGT ATGTGGGGCTTTTIG
EST13518 2	39 A G CTT		G	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTGAGCATTTT[A/C]ACTTTAAAAATTAACCTCA ATGTTCTCGGAGTCGCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGTATIG
EST13522 8a	45 C G ---		---	CAGTTGGTGATTCTCAACTAGGAGCTATTTGCCCCCATCCCCCAGGAGTGTCTGGAGAC[A/ G]GTTTTGATTGTCACAACTCGGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	66 A G ---		---	CTTTAAGGAAGTGAGCCAGATGAATCCAAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAAGGAGTTGCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAATGGT
EST13785 0	69 T C ---		---	AAGATTACGGACCATAAGAACTGCCCCCGGACCCATACACACAAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAA[A/C]GTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	101 C G ---		---	CCCTAACCATCTGTAAACCCGAGCCQ[G/C]AGTGACCGGGACTTGTCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	25 A G ---		---	CAATGGTGTCCATGTGAACATAT[A/G]ACCTATTTCATAAAGTTAAAAATATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGAOCGAACAGGAGGGTAGGAGG
EST14221 5	23 A G ---		---	AATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTA[T/C]TTTTGAAGATCTTTTAAAAAT ATTTGACTTGTTCCCTTCACACTCATTTTAAATGT
EST14812 2	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAATCTTTAGAAGTCCCGAGTTGCCCTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	50 A G ATA	CAAGTCAGCTT CTACATTTCTGA	TAAAGATTAC TTAAATCCCAT TATGTACT	TTTGCTTCGGCAATACATAGTGGCAATGCGAGGTGAGTTCGCCCGTCTCCCCACTGAACAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAAGTTGCCCGTCTATCACCCACTACTGGTT[A/T]TTCC GGTACTGTTTCCCGTA
	128 A T	CATCACCCACC TATACTGGTT	CGGGAAAACA GTACCGGA	

EST15420 6	109 C A ---			---	TTTAAACCCCAAGACCTTGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCAATCATATAGCCAAAGGACTC/AJGGAAATTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAGAAGACAA AGACAACAGAG TTATTCTC	GAATAGCTGA AACAGAGATA TTATTCTC		GTCACCAGCACCTTTTATTAGACGTGAAAGACAAAGACAGAGAGGAG/CJAGCAGAGAAATAATA TCTCTGTTTCAGCTATTCAGGATGTTATGCCAATTATCCAGAGTCCCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	GGTTTGCCAT GATAGTTGATG	TTCAATTATCC CTATAA		AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTGCCATCACAAGC/GAJTTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCATAATTCCTCCAAAGGT
WI-16782	96 C T CACTGTAAGG	GGTGGAGTCT TC	CTTCTATCTTT CTGTTCTCCA		CTTCTCTCTAGACGTGGAATACACACGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGAGTCTCACTGTAAGGA/CJTGATGGAGAACAGAAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATGTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA	G	AAAAATGTAAACCTTAGAGGTTGCCTCTTTTGTGTACATTTTCTGTGAGATGCTTTTACCTGAG/A/GJ CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---			---	CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTGAGGCAACATAGGA/T/CJGTGA CAGCACCACTCGGACCAAGAGTGTGCTGAAATCGTCACTAGCGTGCCAGCCCTTTTTCCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89 G C ---			---	GGTTTGAAGACGCGAGCTTATCTCCACCTGCCACTGGGATTCTCATTTTGAGAGCTGTTTGTGAGCC TTTTCCAGAAAAGGCCGCTC/GCJGGGTTTTCTGAACCCCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---			---	CGTCTGAAGTTTTCTTTATCACAAAGTCACATCAATCCCTGGGGCCCTGCTCAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTC/CJTAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---			---	ATCCAGCTGTGAAGGGACAGGAG/CJGJTAACACACAGTCCATTTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTGTTTCACTCGTCCATGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---			---	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCCAGGGA/GJTTGGCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---			---	ATGGTATAACAAAATCAGTCCAGTTTTTTC/GJTGAAACAAATGATCCTTTGGTCTTTCCCGTGGC CTCCTAAACAACTAAACACCCCTCTACGTCTAATCAGTCACTAACATGATCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---			---	ATGGTATAACAAAATCAGTCCAGTTTTTTC/GJTGAAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACTAAACACCCCTCTACGTCTAATCAGTCACTAACATGATCGAGTGGCAAGT CTTTCACA

-200-

EST16151 2	53 C T ---			AGCCAAATTCAAACGAACTCTATCAAACACACAAAGGCCCTAGAGGAGAGATTAC/TAATGAACGT AAATAATCAAGGCAATTTTGATCTAAAGCATTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGTAGGAAAGATAGTAGTGCAAAATAAATGGTAAACACGACAG/GAJAAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTTAAATTTATTTACTGAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b				GCAGGTAAACTGTGTTTACACACGTAATGTTCTTTCATAAAGAAAGAAATATCTAGTTG/A/GJTAG AGGAAGGCACGTCTTCCCTGGCCCTCTTCTGTTTCATATTTTATGTCACTGTCTAACGTTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAAATCA/GAJTACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAGTCAGCATATAAACACATGGGTACATGCTCACGCACATGGTGTG
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGTGACAGATTTTCATT/CJTGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCCACTAGCTGATTCAGACAGGACAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGTGACAGATTTTCATT/CJTGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCCACTAGCTGATTCAGACAGGACAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGGTGCACATGCACATCCTTGAACATATCATTGGCAA AGGGAATGGGTATCAAAATGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA/GJACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCTGTGGCTTGTCTGTCCAGCTGTCTCCAGTGCAGCTGCCACA/GAJTGGTCTAGCCTCATGG CAGAAGCATTTTAGCCAACTCTGTCTGTCTCCACTCTCTCTCTCCGCCGCTGGGGCTCACCCACC TCCTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG/GAJCTTACACCTTTAGCACGGATAGTTTCTGTGTCCTCCAAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	TTCTTCATAAG	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTGTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGCTTACACCTTTAGCACGGATAGTTTCTGTGTCCTCCAAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTTAAATGAACCTT/CJGGAATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCTCCAAACACACACACAAATAAGCAGCTAATGGCAAT/GAJCTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAATGTTTCTTCCIGATATGAGGAGAAATCTGCTCTTTATGTA

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WI-16879	79 C T	GATACAGGCC ATATTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCACTATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCACTCTTAGGTGGGAGAGACAAATCTCCCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTGACAGGCGGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTTG	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGAGAGAGAAACCAATGGAACGGTAGCTAACTTTGGGCAGG TTCGAGTTAAATTTGGTCAATTCAGAACATTTCCAAAT
WI-16905	75 C T	ACTTGGCCTGT GTTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTGTTGTTTGTATTTGCCCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCACTCTCCCACTGCCTAGAGAGATATAGACA
WI-16910	74 G A	AAGAGTAAAG ATGGCGTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAAGATAAGATGGCG CTAGAAAGAGTATCTGTTATAGAAACGATACITTCATTTGGGCCTGAACCAAGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATCTCTCTGCTACACAGAGCAGTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCACACCTGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGCTCATGGAATAGGCCTGGAGCAGCAGGATT TGGCTGAGGCTTCAACTGACATCAGACAGAGCTGCAATCAAGGGAAGCAGACCTGGGGAGCJCCA CGGGCAATCAGATGAGATG
WI-16947a	58 C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGCTCATGGAATAGGCCTGGAGCJGACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAGAGCTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAAACACCTAATATTCJCTTAACTTTGGTCCAATATTT AGTATAACTAATATGAGTTTATCTACTGATAACTTGCAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTGAGTCCAGACATCAAGCATAGAAAGAGCAGTAGAGACTGAGGTAATAGTATTTTCJACGGCTGG AAATCAACATGCCCTCTCTCTGTGAAGTTGTCAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGCACCTCAGCTAAGCACCAGAGAGTACACTGTGCGCCCTCATCTGAGATTCJGTG TAGGACTGTAAAGGAATGTTTGGGGTTTAGGAA
WI-16992a	46 G A	AAGCACCAG AAGTACACTG TC	CACATTCCTT ACAGTCCCTACA C	AAATACATGGTGCACCTCAGCTAAGCACCAGAGAGTACACTGTGAGJCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCACAGGA	AATAATACGGT GTTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGTCATGACATTCAAACACCCGTTATTATTAGAAGCTCATTTAAT TGTTTAAATGCAGACAAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTTCACAG
EST17127 9b	74 C T	CACTCGGCAC AGACAGAGT	GGGAGGGCAGG GGTG	ATTCCGTCTCCAACAGCATCCACAGCCGGGATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGTC/TJ/JGGGAGCATGGGGACCCCTGCCCTCCACAGGCTTCTTAAGTAACAAT
WI-17040	94 T C A	AATTCTCTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGCGTTCATTAAATTTGGTACAAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAAATCTCTTATCATCTCAAGCCAGTC/CATCACTGAATAAGCCATAGTCCCAGTCTCGTTTCC AAATCTTCTCATATGT
WI-17044	47 G T G	GCAAGGGAT TAACGTATAG	GGGATCCCT TGTTAAGA	TGTTTGTGTTTTCTCTCTCTCCAGGGATTACGTATAGGTC/TCTTAAACAAGGGGATC CCCCACTTATAGTCACAGCAGCAGCTGCAACCACTGACTCTCTGCAGAAATGGCAGGGAATCGAAT CAAAAAGAAAAGCAAGTG
WI-17021	62 T A ACTG	TGGACTTGTC A GCCTATAACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCCCTATAACTACTCT/AJG CAGCTGCCACTAACTCTACAGGCACAGTAACCTATACACTTTATACAGGACACATGCCAAAGTGCCTGG GAGGTGCCAATAAAATCAA
WI-17065	90 T C CTT	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAAAAATGTAGACATGGGGGAAAAAACATTCGTAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAAGGAAAAGCATAAACTTC/CJAGGATTCATTGTCTCTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGTT	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAACATCACTGTTT/CJATTCCAGAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATCCCTGTAGTTCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G ---		---	TGCTGACTGTATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCCTCTACACAGGCCTC/TGJCTACATAGGAGTATATTGGCCAAGACTCACCACTAGAAAGTGATT
WI-17104b	108 T C ---		---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCCTGATGCTTTCGAGCTTTCCTCATTCCCA AATCAGAAGCAGTCAGTGGCCCCGGTTCCAGACGGCTTC/CJCTCTTTGTTAAGAAATTA
WI-17114a	37 T C GACTTTGTTT	TTCCATCAAG GACTTTGTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTCCATCAAGGACTTTGTTTT/CJGTCTCTTCACTCTGCTATTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGTCTAAAAGAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T G CTTT	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCCCTCTTC/CJCATATCTCCAGGATTCGAGAGGGCTCTCTTGTCTGCTCTAATTT
WI-17163	43 A G TAACGTT	CATTCTTTGT AAAATAACAA	CAGAATCTTGC TTTTGCCTT	GAAATCGAATACGTCCATTTCTTTGTAAAATAACAATACGTTT/JGJAGGCAAAAAGCAAGATTCTG TAAACCAACATTGGAAAAGGGGACACAGGGAGGGGAGGGAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

WI-17178	127 T	C	GGACTCCCTCA	CCCTCAATTTT	AGCAAATGTCCTCCCAATTCATTAGCTATGATGGAGTTATCAGTTTCATTTTCAGAGCGAATTACTGG
WI-17180b	81 C	G	---	CAACTGCTTC	GGCAGGGGGTTTAAATATCCTGATGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T	C	TGCA	---	GCAGTTGAAAATTGAGGG
WI-17180b	81 C	G	---	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTCCTCCAAAGTCGTCGCACAG
WI-17180a	47 T	C	TGCA	TGCGACGAGAC	GCCTCAACAATTAC/JAACATCTTGCCCATTTTGTTCATTATCCGCCACCCACACTGCACAGATGAG
WI-17156	54 G	C	TOCCA	TTGGG	GGAGTC
WI-17149b	79 T	C	---	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTC/JCCAAAGTCGTCGCACA
WI-17149a	48 C	G	AGGAGGAACA	CAAGAAATAT	CAGGCTTCAACAATTACCAACATCTTGCCCATTTTGTTCATTATCCGCCACCCACACTGCACAGATGAG
WI-17197	67 G	A	CTGGGCTAC	ATATTTGATTG	GGAGTC
WI-17198	38 A	C	CCTAGTTT	TGTTGGAA	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATTC/JTTCCACAGA
EST18753	27 C	T	GGTCTCAT	---	ATCAAAATATATATTTCTTGGTTGGAAATTTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT
WI-17108b	74 C	T	CA	CCACGACGTG	TAATATCTTG
EST19067	41 A	G	---	CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATTC/JTTCATGACAGTGCCTG
EST19067	40 A	C	TTC	GCCTGA	GAAACCCAAATTGTCATGTGATGAACACTACAAAAGGATGGGAAAGAACACATTTTCTCTACA
EST19125	28 A	G	---	AACTACGATTT	ATTTGCTATGTTGCCCTGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAATAGTGGGGCTAC/G
WI-17108b	74 C	T	CA	ATCATATGCTC	/A/GGTATGCACCACCTCACCTGCTTATCAGTTTCGTTTAAATAGAATATTTGACTTTTAGATGCGCA
EST19067	41 A	G	---	OC	TGTATTTTCAGTACTTTTCTCCCTGCTGCTAGTTTTC/JTAAATTTCTCAGTGGACAAATGGACAA
EST19125	28 A	G	---	---	ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
WI-17108b	74 C	T	CA	OC	ITC
EST19067	41 A	G	---	---	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGGATCCTCCTGCCTCTGCAGTGGCTGG
EST19125	28 A	G	---	---	GATAAGACACAACCTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
WI-17108b	74 C	T	CA	OC	TTATTTTAAACATAACCAGATGCACCTTGGTTTTCATTCTCTGTTGCCATTGAGTCTCAAAGT
EST19067	41 A	G	---	---	AAACAC/JTGGAGCATATGATAAATCGTAGTTTAAAGAACCATAGCATTACAGAGT
EST19125	28 A	G	---	---	ACACAAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JG/JGTGGCATTAAGTACATTCAACT
WI-17108b	74 C	T	CA	OC	TTTTGAGCAACCCGCCATCACCAATTCATCATCCATCTCCGTT
EST19067	41 A	G	---	AAAAGTTGAA	ACACAAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JC/JAGTGGCATTAAGTACATTCAACT
EST19125	28 A	G	---	TGTACTTAATG	TTTTGAGCAACCCGCCATCACCAATTCATCATCCATCTCCGTT
EST19067	40 A	C	TTC	CCA	CTGTTTCTCAGAGATGACACTGCCAACAJA/JTTCACAGATTTGCATACATAACAGTTATGTTATGGC
EST19125	28 A	G	---	---	TATTCACAAATTTACAGTAGTGTGTTTTTCTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATCAAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGTAGTAGAGGGCCAGTAAGTCGGGAGTGTCTGATTGT/GTJTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCT/G/GJTAGCACAAAGTGG ATGCTTGAAGAAACTCAGTCTTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128 G A	TTCAATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGGGTCTGGGAGCAGGTGGGCAGTTTCACTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCATATGGCCATTTTAAATAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGAAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAGAAGAT CTGTCTGGCATTCTTTT/GJGTGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGGGGT	GTTTAAATGATCACTCACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCTGCCAT/GJACCGCATCCTTCATGGTAGAGTATCAAAAGTAAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATCAATGGTTTTTACTCTA/GJGTGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCC/GJCCACTGTAAA CAGTAGCAATCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAAT/GJACATAAAAAATCCACCACCTGTAAA CAGTAGCAATCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGC/GJACCAAGGGACGTGTGCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTAACTGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCCTTTGAGATATGATGAAAAATATCCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC/GJGTCTGTAGTTAAGCTGAAGCTGAAATTT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA T	GCATGAATTTT	TATCCATTTCAAGAAAAAATGACTTAAAAAATACAAATTTCTATCCAGAAATGGATCCTTATCTG CACAG/GJCCATTGAAGAAAAAATGCAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTGTT TCTACCCC	TTGCCTGTAA TTTGACTGTAA TG	GCCTTTTATGTCTCTTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTACCCCA ATT/C/CATTACAGTCAAAATTAACAGGCAATATAATAGGCTAACAGAAATGCTTGCATTT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCAATTTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAATCTTTGCGCTT/AJATGGTTTGACAGTTTGTGTCTTTCT T
WI-17387	55 C G	CCTTTCAGAT TGAAGAAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAATTTAACATGCAAGTTTCATTTACATTAACCTTTCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTTGGCTTGTCTGCAGAAATAGATGAAAAAGAGAAAAATATACCCAGATACTTTGTCTCACTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG/A/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G	GGCTGTTAGTT TTGTTTGT	TGCACITTTAA TCCCATCAAT	AAAGGCTGTAGTTTGTGTTTTTGTCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCAAGGCTAGAGAAAGATATGAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGATACCCACCTAA
WI-17470	83 A G	GTCCCGTCCG CCAG	CCAGTGACGAG GCGA	CTGACACGTCCTGTGTGCGGGGTGTCATGTGCGGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCACGCCCT/A/GJTCGCCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCGCTTCC
WI-17519	55 T C A	GTGTCTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTTGTCTCTAGCTAATGAATGCA/T/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTTCTATTTTAAAGAGCTTAGAACAAGTACATGGTGCATAG
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAAACAGTTTGTAACTATTTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCCTTGATACAGGTAAACAGTTTGT/A/CJACATTTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA/C/TJTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGGCGCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAAT/C/GJATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CAITCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGAGTAGGAGAGGCGCTACT TCCCTTGTGTAACACTCC/C/A/GJATATTGTGCGATTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGTC

WI-17623	46	T C ---	---	TGTGGTTTAATTTAAATTTCCCATATAATTAATGGTGGGCACATTT/C/GCATGIGCTTACTGGGTC ATTCATATATCTTTTGGAAGCATCTGCTCCAATCTTTTGCTGACITTTGGAGTTTTTGGT
EST26419 1b	46	T C ---	---	ATTTACATACAGAGATACAAAAGGCAACTATGTGCAGCAACAATCTGA/T/CJGGGCAGTCCAAAATCTCT TGGAGGAAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35	C A AG	CAAGAAGTTTG GACTGCCC	ATTTACATACAGAGATACAAAAGGCAACTATGTGCAG/C/AJACAATCTGATGGGCAGTCCAAAATCTCT TGGAGGAAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69	G C ---	---	TCAGCTTTAAATTTAAGGGACATGTAATAAAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAAGC AG/GC/JAGGTTAGACCCAGTAACAACAACCAAGAAAGCAAGTGCTCGTTTCCATCTTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39	A G ---	---	TACTTCAGITTAAGGCAAAATCCACACAGAGACTGTCTC/W/GJGAGACGGGCACAGAACCCAGACACC GTAGAAACACACCACCACCATGATGATGACGGGAAGCAGAG
EST27152 1	101	C T ---	---	CAAAGGATTTATTTTGTTCCTTAAAAAGTAAATCTAGAAAATAGCAACCCACTGGAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCT/C/JTTTACATGGTGTACTCTTTCATGTACACAT CATCGGAAAAACAGACTGA
EST27504 0a	33	G A ATTT	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACTTTGCAACAATTTAAATTTATC/G/AJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTTACACATTTCTGTTAACAAGAACCCCATACATT GGTAAATTCATTCT
EST27662 4	51	C T CTCCAGTCTTG	TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCTGTTCTCCAGTCTTG/C/JIAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT
EST27788 3	100	A G ---	---	ATTTTATTAGCGGTACAAATTCCAAGGTGGTAAGGTGAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAAACAACTTTACATTTCAAGGAC/A/GJGCTTCCAGACAAGCCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58	G A AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCCTTAAAAACTTTCTCTGTTGGATCCCAAGTAGCTGGAAGTCATCAGAACCCCAAC/G/AJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58	G A ACAATC	TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTGCACACAATC/G/AJAAATG GATAAGGCTTCTTGACAAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37	T C ---	---	TCCCGCTTCCAAAAGCTTTATTGGCAAATATGCTCTAT/JCJAAAAGAATGATCAATCCTGTTGCCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACGCCGTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTCTCGCAT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTTCTTTAAAT[ATATGGTATAAAATAAATGCAGAGAAACATTAAC GGAGATGTACAGACAACAGACAGATGAGTTTGTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C TGTC	TGGGOCCTCC TGTC	TGGTTGGCAG TGTC	AGAAATTGGTCTAGTAATCGTTCAAGATTTCGGTGATGGCCCTCCCTGTCT[CGGACACTGCCAACC CACAGCTGGAGGGGCATTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68 T C	TGAGCCTGGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTACATACATCAACCAAGTGACATACTG TTT[CACATGATTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGTGTCA
WI-17730a	39 A C ATT	GACCACAGAA GTGAAGTGCT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACCACAGAAAGTGAAGTGCTATT[AC]GTTACATACATCAACCAAGTGACATA CTGTTACATGATTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGTGTCA
EST29041 5b	53 G A CA	GGAACAACA CATTAAAGCAT	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAAACACATTAAAGCATCAATTGTCAC[TG/A]GCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	CTTTAGAAGGACACACAGTCTTGTGGACTTAGGGCCTACCCCTATCCAGCAGGTGCC[AG]TTATTT TCACTTGGTTACGTCGTGAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T ACAGGCT	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGAGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[CT]ACAGAAAGAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	TATTGGTATGCTTAGGGAAGATTCTGATTAGAGATAATTAATCTTAAAGTTAACTCACCATGAAA TTTAAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[GC]JAGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	AAATAAATACATCATGCGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTAATAATTCC[A/G]GGATTTAATTTCTCCTAGTTCAATCTTGGGA GG
WI-16250b	86 G A	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGAAA[GT]ACCC GTTTCACAATATAGTAGC[GA]ATAACCCAGGCTCACCTTCCCTCCGTTCCGTTGAGAACTTCGTGGGAC
WI-16260a	59 G T A	TGAGGTGGATT CAAGAAGAAA	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGAAA[GT]ACCC AGAGTTTCACAATATAGGTAGCGATAACCAAGGCTCACCTTCCCTCCGTTGAGAACTTCGTGGGAC
WI-17835	30 G A TG	ACAGGAAATA TTGTGCTTTCT	TGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATAATTGTCCTTCTG[AG]GCTGTTTCTATACCCCAATATCATAGAATT GTTGTTGCTTCTATAATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAATGAATTACCTGAATT TTCTCCTCTTGTTCAAA

EST31951 4	87	C T	GGGTTGTCCAG CCAACA	CCACCAAAAT CACTCC	ACAGCCATTATTATGTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTAGCAATGACA TCGGGTGTCCAGCCAAACA/C/TGGAGGTGATTTTGGTGGGAATTTCTATCACAATTTATCT
EST31968 8b	95	T G	---	---	CGAATTTGCTCTCTTATTTTGTGATCTAGTAATCCTAAAGATTTGGGGCGGGTTACTATAAGT GCATTTTATAATGGGATTTCTGCTT/GJAAGTCCCACTGATTTCTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGCAGTT	CGAATTTGCTCTCTTATTTTGTGATCTAGTAATCCTAAAGATTTGGGGCGGGTTACTATAAGT GCATTTT/GJATAATGGGATTTCTGCTTAAGTCCCACTGATTTCTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACCTCCCTCCGACCAGATGCTGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTCAGGCCCATTTGAATAGCAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGGCTTCCAAGCATTCAAAGGCACCTTGGGTGTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCA/G TCTGTATTAGGGAGCACCCCAAGCCAGTAAACAATATGGTTC/TGCAG
WI-17800	29	C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTTAGGAAATATTTACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCACTCCTAAAGTCTGGGATGACTTTCCTT/GJATTCATACATCAAGTAGAACCTAAGCCAA TCAGAATCAGAACTCCTTTTGTCCATCAAAATCCAGTAACTCCAGCTGAATTAATGTTCACTCT
WI-17860	121	T A	TTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAAACCATGGCTGTCAATGATTAATTTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAAGATAATTAATTTCTGGTTTAAATCTTTGCCAGCAAGCAAAATAT/T/JCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGT/T/JTTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAAACTACCA
EST33301 4c	80	G A	---	---	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACACAAGCATGATC AATCGCCACGAGA/GJA/ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A C A	AGCGTGGTTTT CAATACTAAA	CTGATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTCAGCGGTGGTTTTCAATACTAAACA/G/A/JGTAAACAATGCAAAATAT TAACAATAAATACAGTGATTAATAAGCCATGGCATATCCAGTTGATGTAAATACTTTGCAA

WI-17904	50 A	AAAGCATGAC AATAAAATGA ACAC	CGTTATGTTA ATAGTAATTCC GG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAATGAACACAG/GJTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACAAACACAAATGA
EST34149 5	69 A	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAACTA ATAAAATC	GTITTTCTTTGAGTGACAAAGCTGTTCATTTTGAGAAATGTGTGCCAAATACTCAAGTGTGAA TJAG/GATTTTATTAGTTGTTCTCGCTAGTAGTTTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTTC/JATACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGCCATATG ATATATAACT CCTAAAAGC	CAGAAATTATG TGATAATAACT CCTTC	GGTACACAAATTTTAATGGAAGGAACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTCTAAAAGC/JTGGAAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACTCGGGTGTTAACTGCCATTATTGATTATTTATGATAAAACAACTCTCATTTGTGA AAACAGCTAAGGGTGACATCTCCAGACCCCAACCACCTGTCCTGTATGTJAC/JCTGCTGAGAGTCC ACATTTTGGAAATCCAA
WI-17996	84 A G	GTAGAGGCGA AGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGTTGGAAGCAGCATGAAACACATCTCCCCAGGCCTCGCAGT AGAGCGAAGGGAACAG/JG/GCTGCCATGTGCCTGTCTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGAGACCCGGT
WI-17136	33 C G	---	---	ATCTTTTATAAAACACCATGTCCCTAAAATGTTC/JATTCACATATATGACACACCTTCGATGTAT AGGACACTGATCAAAAAAGACAGAGAAATGTGTCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTCC/JC/JGTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACITTAATCA
EST35164 8a	57 A G	CACAGCCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCTTCAAGCACACGCCCTGCCCC/JG/JCTTGA GATTCAGAATCCAGAGGGTGCTCAGTCTTGGTTAGGTGCTTCTGTGACATTTCCCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATCTTGGTTACACATCTTAG AV/JACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATCTTTCATGTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGGG GAGTAAAA	CGTCACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA/JG/JTGGAAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGTCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54 G A A G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAG[G/A]GAATGTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGCTTATTAGGTGCCAAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAOC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATCTTGATCATGGGTGGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C G T G T A T	AACCCACTAC TTACTCAGAGT	AAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTAT[C/J]ATATTAAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATTTCTGTACTCAGAACATTTAGGTGCAAGGATATAA
WI-18080c	80 C T ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGIG TTTGACTTTTAT[C/J]TCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTCTCCTTTGGTGAT
WI-18080b	65 G A ---		---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGIG/ AJTGTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTCTCCTTTGGTGAT
WI-18080a	41 T C A G T C T C	GCAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCT[C/J]TTGTAAATTAATCTACTATGTC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTCTCCTTTGGTGAT
WI-18086	63 G A ---		---	GTGGCATCCTATAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATCTT[C/G/A] TGGCTTTGTTACACGGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTTGAA
WI-18115b	71 C T ---		---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCCTTAGTGACCTTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T TT	TTAGTGACCT TTGGTATCCC	AGAGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCCTTAGTGACCTTTTGGTATCCC TT[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78 A G ---		---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTA GGTAATTTGC[A/G]TAAGAACAAATAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115 A G A G C T C	CCATCTTTCCG	GAGTTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTTCCACTATGAAGGCAATCTGAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTTCCGGAAGCTC[A/G]TGGAGACAAGCAGA ACTCGTGGGTAGAGTGA
WI-18190b	26 G A ---		---	TGAAAGAGTGCACACAGCGGACACT[G/A]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGACAGGGACAAATCAAGAAATGAGCTGGAGACATTATCCTGGCGA

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WI-18190	62 G A	---	---	TGAAAGAGTCGACACAGCGGACACGTCTATAAGTGGAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTTACCAT TTGTTAAGCTT TTG	GACAGTGAAACATTGAAACACACAAATACAACAAAACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAATAATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACCGTA TGTGTTCTTGAAC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT CCCC	ATTTCATACAAGCATTTCTGAGTACAACTAGGGACAGGTATTTACAAAACAAATAGAGCAGA GTTCTGCCCT[G/A]GTGTGCGGGGGAGAGAGGGGATTTCAGCATTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A A A	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAG[T/A]GAA CCCTGAAACCTTTATTTGAAATGAAATTTTGTCTCAGAACTGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAACCTG AGTTTGAGATC CACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAATGCTTAGATTTCTCAGTATTTATCAATAGTGTGTAAGCTGGAACCTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTTCGGCAGAACTGGC
WI-18242	30 G A A A T C G T A A C A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACACTACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAT TGGATGCCACAACTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAATGTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[T/A]CATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T T T C A A A	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGGA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGCAAAATGATGCATGAATCCACATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTGAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGAGATATGTTAGTGTCTATCATTAATTTTGGAAAGCTGCAGCTATTGTTATTC AAAT[A/G]TATCTTCTGCTCCCTTTCTCCTTTTCTGGATTCTCATTTCTGCATGTGTTATA
WI-18330b	66 A G	---	---	AAACATCTACAGCTGTCTTAGGCCATCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACATAATTTTTTTGTTGAT TCACA

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WI-18330a	49 G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAAATAAAGAACATAATTTTTTGTGAT TCACA
EST37564 5	85 T C A G A	AAATTCAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT[C]TCTCATTGAGGCCCTCATTAGGCTGCAAAACACATCAAAGGCATTAC TGTAAGTGAGAGGAGCTGAG
WI-18327	104 G A T T	AAACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATCGGAGGCAGA GT
EST37624 6b	102 G A ---		---	GTGGCAAGAGCAGCTAAACACACACTATTTTGCATGAACCTCCAAATACGAACAGTGACGCTGATGG CCTGCAGTCTCTGCCGCTGCTTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGGGTCC TCTGACCTCCCCATTCC
EST37624 6a	58 C T ---		---	GTGGCAAGAGCAGCTAAACACACACTATTTTGCATGAACCTCCAAATACGAACAGTGACGCTGATGG TGGCCTGCAGTCTCTGCCGCTGCTTGGCTCTCTGGACGGTTCATTCTACATGGCTGCTGCTTTGGGTCC TCTGACCTCCCCATTCC
WI-18357	89 C G GCATCAA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTCTGAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCA[A/C]GTCATCTTCAGTCTTTGAGTCCCTCCAGCCCAAGGTCCTCAAGCTT GTGGACACAGAGACAAGCC
WI-18012g	117 A G ---		---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGAAG ATCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113 G A ---		---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGAAG ATCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112 C T CCCTT	GCCACTTTTC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGAAG ATCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46 T C ---		---	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGAAG AGATCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75 A G C TCTGCATTG	GCAAAAAGGA CTGATTAAATAA	GCTAAAGTCAG CTGATTAAATAA ACTTAA	CATATCATAGCCAGATCTACAAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGTAGTAAAGTTTATTAAATCAGCTGACTTAGCATTTGGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAAACTGACCCAAATTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACCTTGGT/G/GCTTCCAGAGTGCAGTGATAACTGTTATAGCC CCTGCACCTCCTAAAGATCTTTTCT/TTCCCCAAGTCTTACAGAAATGGTATATTCCTCTGGAATA AGATGAAGTCATCAATGGATTGTGCTCTCGTTCAGCTTTGATTTTTTTTGCTTGGAAACCTTG TCCTCCCTGCTGATT
EST38519 0	24 C T	GAACATCCCA TGTTCTGTTT	TCTGTTAGGAC TTGGGGA	AGTGGTCAAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/C/TCTCTTATGTGTTATACTACCTTCCCTTCTCTTTCTTATACACATAGATTTTCCCTTAATTGCAGC CCA
EST38575 1	66 T C A A	CCTGCTCGGC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTCACGCCCGGGGCCCGCTGG AGTCTCGCGGGGCCCGCCCTGCTCCGCCCTTC/G/GCCACCATCCATTCTCCAGGGG
EST38616 9	101 C G	TCTGAACCTGGG CAATTCAA	TTGCAAAAAATG AAGGAAAAA	TATAGTAGGTACTTTCCTTGTGCTGCAGCAGGAATTATTCAGTCTGAACCTGGGCATTTCAA/T/CJGCGTG GTATTTTTCCTTTCATTTTGCAAGTAAAAAATCAT
EST38652 8	59 T C	AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATAT/CJAGATAGAAGATTAAAGGACCAT CACTGAGTCAATAGCTCAGAGGCAGATTAAAGATTGGACCCAGGAGGTGGTCCAGCATATA GGATCCTCACTCACCTGGGACAGCCTGAGAAAGGACATCCACAAAGACCTACTGATCTGGAGTCCCA CGTCCCC/GJAGGCCAGCGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATCTTGTCTTCTGGAA
EST38707 9	75 A G	---	---	ATCTTGTCTTCTGGAA
EST38759 2	86 A G	TGTTCTCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATCTTCACTAGAGGGGAGAAGATCACCTACCTTTTGGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG/GJCTTAAAGTCCAGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCAC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCCAAAGAGAAAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTATGAGTATAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTATGTGTGTTCAATCAACAAG TGTTTATGAGAACCCATTACACAG/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T	CACGAGTAAA AAGAAACTCA	GGAGGAGTGC AAGGAGAA	TCTTTACTGTGTTACAACCTTCTCCTCAAGTTTGGGGTGGTTCCATATTTGTTATTGTTATTATTA TTCAACACGAGTAAAAAGAAACTCATGAC/C/TJTTCTCCTTGGACTCGCTCCTCCTCCCAATCTCGAT ACCGACTGCACCTGTG
EST38865 2	72 T C	GCTGTAGAATT TGTCGATGC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTGCTGTGTCTCTGAGGAGCTGTAGAATTTGTGTGCG ATGCT/CJCTGTGTCTCCTCGCTCTCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTATGTTTAA

EST38878 9	47 T	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAA[T/C]TGAGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTTCCC TTATTCATGTCTCATCTACACATTTCTTTATTTTATTTTATTTTACATTTCTCAAAATATCGGATTTGTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGCGAGTCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TGTCATCTCAC ACATTCCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCATGTCTCATCTACACATTTCTTTATTTTATTTTATTTTATTTTCTCAAAATATCGGATTTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATTT TA
EST38909 5	35 T C	GCACAGCATG GCTAAAACG	GGTATTGTTG ATTCCCATCTT T	GCACATAACTAATCTTTCATTTGTGGATTGCACAGCATGGCTAAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAACACACTACACATCAAACTTAGGAAATGTGGTTAGTGTGGTACGTTGAG GGAACCTTATAACCTCAC[A/G]CGCTTTGTTTCAAAAACAACAGCAGACAAAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	TAACATTTCCCATTTGAATTTCCCTTGGTGGG[G/C]GGGGGGGGGTGAGATTGCAGTGTCTCAAGATAAA TATCACAATATATCAAAACTTTCAAAATGCTATGCAATTCACACACTGACATGAGCCACAAACATTT CCTTTCACAGGGACTGTAC
EST38955 5	30 G C	TGAATCCCTT GGTGG	CACGTGCAATCT CAOCCOCC	CCTGCTATGATGCCTGGCAGATCCCGACCCCTCGGTGAC[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CACGTGGCCCCCTAAGTTCCGGGTCTTCTCAGTCTGATGGCTGTGTGGAAAGCTTGGTGGTAAG GCCTAAGGAA[T/G]AGGGGGCAGGGGGCGATGCCCGCAGCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CAGC	AAAGATAATGTCTATCACAACCGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCCTAAAAAT CCCTATTATTCATGATATTTTCA[T/C]JAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	TCA	TTGATAT	
		CCTTTGTCTC AATTTTAAAG	TAAGGGCTAAT TCCCTATATAA	GGTTGTCTTTCATGATTTTCTCATTTCCCTATCAGGTTTCTGGTCCCTTGTCTCAATTTTAAACACTT T/C]TTTTTATATAGGGAATTAGCCCTTAACTGTGGTACATGCTGCCAAAATTTCTCCAGTT
WI-16403	69 T C	ACT	AAAG	
		GCTTAAATGGC TACAGAAAGA	CCAGAACCCAG ATGTGTTTAAA	GCCTTAATGGCTACAGAAAGG[C/T]GGTTTTATTTTCTTTTTTAAACACATCTGTTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGTGCCCTGAA
WI-16406	24 C T	AGG	AA	

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGATAAACTTCCCTGCTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAATATATACCTGGCAAATGAATGAGGTGTCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAAATAA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTTACCCACGCC AGCTCTGCTTGCTGTCAT
EST39366 2	72 T C	---	---	AGAAAACATTCTGCTGATCAGAGGAAGATGTATGTAGAAAATCAGAAATCGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGAAAAGAAAATGTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCA
EST39371 9	86 A G	CATTGGATTA GCGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCATTTTTCAT TTGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAAATGCTTCTTCTTAAAGATT GACATTGCCCAACCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTCTTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCACGAAGGCCCTCCCCGTACTCTCCCCCTGGAA G
EST39428 8	31 C T	GCCTCCCA ATTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCCCTGGTTGCTCCCAATTTTATTGTTGTTGTTTCTTCAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGCTAGGTAATCTGTTGCCCTTTGGTCCACAGAGCACAAATTAAGAAGATCAGGTCT GGCTGTTGC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/J]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGGACTTCA GAGTAA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAAACGTCAACTTTTGGAAAGAAAATAACAGGAACCTATTATAT ACGTAATCACTTTTATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACCTGAACAGAAA TGCAGGAGGTGGC[A/G]AGAGGGGCCAGATTGGGTGTTTCCAGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCTCT GTAGACATCT AACATTAG	CAC TTGCAATT CTGAAGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTGAGACATTTCTTGACCAAGCCATAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI- 18387b	84 A C	---	---	CACAAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTTGTGACCCCATACATTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGAOCCCATACAGJTITG GTCACATGCTTTAGCCATACACATGTAACATTGACTATGGAGCTTTGTGAAAGTGAATGTGCGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GCGTGGACCT GAAACAC	TTCTTGGAGA AAGGCGTC	TCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAAACACAGJGJGACGCCCTTTCTCCAAAGAGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTTCAGGAT AGGT	GCACACCCCTC ACACTGTTA	TCCATTCAAGTATCACATCTTCAGGATAGGTJAGJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTTCCGAGAGTAGCAGTTGTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGGA CA	AAAAGTGAATT GTTAAACATG CTAC	ATGTCATTCTGGCTTTATTTTGGACACJGJGTAGCATGTTTTAACAAATCAGTTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTTCACAAATTTTCATCACTGTAAATTTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATTCTCAGC ATTGCTATAAG C	AGAGAGACAACAAGAAAGAAATAGGGAAATGGGAAAGAACAGAGTGAATTAAGCAAAATCTTGGA TTCAAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAJGJGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTC TTTAATTTCAC TC	AGAGAGACAACAAGAAAGAAATAGGGAAATGGGAAAGAAJGJTAGAGTGAATTAAGCAAAATCTT GGATTCAAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTGCT AGACAGATTTC A	---	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAGGAAAGATCAGACACCCCTGTC CTAGACAGATTCAJGJTGACACAACAACAGGAGGTGGGGTCCAGTTCCAGTTCTTTTGGCTTAAGTGGGACTAJGJTC TAGGGC
WI-18425	81 A C	CACCTGTGCT AGACAGATTTC A	CCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAAGCCAAAGATCAGACACCCCTGTC CTAGACAGATTCAJGJTGACACAACAACAGGAGGTGGGGTCCAGTTCCAGTTCTTTTGGCTTAAGTGGGACTAJGJTC TAGGGC
WI-18449	129 C T	CTTTTGGCTCT AAGTGGGACT A	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACATAAAAAAGGAAAGGAAAGAGAAAGTAAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTCCAGTTCTTCTTTTGGCTTAAGTGGGACTAJGJTC TGGATACAGTCAGGGGAG
WI-18457	120 T C	---	---	ATCGCTTCAATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGGCCCCCAAGACATTATTTTATTCCTT AAATGTCCAAATATCTGCCTGATGCTGTGTTTGTGCACATTGGGGCCACAGJGJAAATAGGCTAAA AGGAGTCCCACTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA A	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGTCTGTTTACACCACAATGGCAGAGGTGAJGJTAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCAGAGCAAAAGTTTGTAAATCTCGGGTTTAGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGC GAGG	GCACGATGGGA GTGAOC	TGAGGACGTGTGACAAGCTCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGTGGCGAGGJGJGGT CACTCCCATCGTGGCCCTGGCCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109	GA	AACAAATGGT AGGTGGTATT AATACTATT	CGTGTGCATTT TC TTGTAATCC	CTAATGAGATGAATACATGAAGGGGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA CGT
EST50757 b	79	CT	GAGCTCGAGG CTGCTTCT	ACCCCTCACCC GGCC	AGCCCCCTCACCTCCTCTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTTCTTTTATAT GTGAGGGCC[C/T]GGCGGGTGAAGGGTCAGAGA
WI-17675	103	TC	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAAACTAAACATCTTACCAGGTGCTGAAGAAAAGTGCTTCGTTTTAAT TGCCAAAGCAGGGATGTGGACATTTGGATGGTGACTT[C/C]CTGGGTGGTCCCCCATAGATTACCCAT TGCCCTCTAATGGTGCTA
WI-16543	67	GT	AGATAAACTA CAATTTGGGTTT TGG	GATTTCATATT ACAGGGACTT	GATCCATTACCTAGGGTAAATTTCTCCTGAATGTCAACAAAGAGATAAACTACATTTGGGTTTGG G/TJAAGTCCCTGTATGATGAATCAAGAATCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	CG	GCCAAAAAGG TTGGGGA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCCTCTCCCTGACCCCAAGTCCATGGAAGAAATGTC TTCCACAAAACCGTCCCTGGTGCCAAAAGGTTGGGA[C/G]TGCTGGTCCGTACAAAAGTAATT G
WI-17690b	79	AG	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGATC	ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG/G]ATTCCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	CT	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG/G]ATTCCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 a	39	CT	ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG/G]ATTCCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST53012	97	CT	TGGTCACTTTG GGGCC	GGGCTGCCCCA GGCC	ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG/G]ATTCCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST53349	96	AG	TGTTGAAAGC AGTCACAATG GTAC	CATCTGGATAT CTTGTCACATT TT	ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG/G]ATTCCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST53389	74	AG	GGAGACCTGC AGAACTTAA CA	GCCCTTCTAA CAATAAATGCT C	ACAACATGTGAAGAAGATATGTGCTTTACTACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG/G]ATTCCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG

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TGR- A003P30	117	C G	---	---	ACAAAGTTCAAAGGAGAACCTTCCTTTGTTTTAATGCAGCTGTGCTCAGAAAGCCCTGTGATTTTCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA/C/GJACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TGR- A004S34	156	C T A	CCAAACCTCCT CATTCTATAA	TTAAA	GCCTGCTTTTATGTTTAGGTTCCGGGGAAGGAGGGCTGACAAACGAGACATCTGGACACACAGC AAGGGTCCAGGGAGGTTGCAGAACCTTCTTGCTCTGGCTAACAGTCTGTGACATAAGCCA AACCTCCTCATTCTCTATAAA/C/TJCTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97	A C	---	---	AACAACAGTGTAACTCTTTAACAGGGGATGTTAAAGGTAAAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT/CJAAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAACAAATATGACTTAGCAAAAGAACAAATATAG
TGR- A004T44a	69	G A TGA	GGAAGATAAA CCAAAATGAT	GCCATGCAAAA TTCCTTATCA	AACAACAGTGTAACTCTTTAACAGGGGATGTTAAAGGTAAAGTCAGGAAGATAAACCAAAATGAT TGA[G/A]TATGATAAAGAAATTTTGCATGGCGATTAAAAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAACAAATATGACTTAGCAAAAGAACAAATATAG
TGR- A004V08	60	T C	CAGGAAAAA GGCATTCCTT	TCCTTCCCACA AAAGGC	CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAAACAGGCATTCTCTTA/T/C/GCC TTTTGTGGGAAGGATCAATTTGGGTGCATGCACCTTAGGGGACAAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TGR- A004V26	125	A G	---	---	TCTAGCTATAAGAACAGATTTTAAATTTCTAGATATAGAATTATCCAGAAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTAATCTTCACATGA/A/GJAAAGGT TTCAGTTTATAATGCTTAAATACTGTATCTATTGCTTAAATCTGTATCTATTGG
TGR- A004V28 a	29	A G	TGTTGTGGTG CGATCTC	CGGAGGTTGCA GTGAGC	CCAGGCTATAATGTTGTGGTGCGATCTC/A/GJGCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCAACCCGCCACCTAACTAATTTTTTG TATTTTITAGTAGAGACATTTGTATTTTITAGTAGAGACAGG
TGR- A004X20	25	T C G A	AAGTTTCCCTT CTCTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTTCCCTCTCTCTGTAGGAT/CJGCTCCATGTTACAGTCAACTATAAAACATGGCTCATGT TCACCTGGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGTCTTTTCA GACCAACCGCTTCCTTCAATTTCTTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TGR- A004X30	26	T C	TTTGAAATCTT AGAGTAGAAC CCAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAAATCTTAGAGTAGAACCCAC/T/CJACTCTAGTAATACTTGTATAAAATTAAGATAGTTTT AAACACCTTCCATAAAGAAATTAGGGTGCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102	T G	TTTCAATTTGGGT ATGCAAAACT	CTTATAATTAG AAATTTTCATGA AAGCAA	CACGGTATATGCCTTATATATAGGTATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCAATTTGGGTATGCAAAAC/T/GJTTGCTTTTCATGAAATTTCTAATTAAAGG ACTGTGCTTCTTCTCATATTCATTTCAATTTGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTGCCTAGCTTGAGAGAACAACTGC AGCATTTTCTTTTCTTTTCTTCCGATGACCATCTTTTGGCTGGCGGCGAGCCCTGGGTGTC TCCCATATCGCTGCTCTTAGTGAGACTGAGGATCTGGTATAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGAGGTT AGGAGACT	CAGGGCTGCGG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGACAGCCCCCAAGGGCCAGGTAGCCTTCAGGGGGGGGCA GGGTTGGGGAGGTAGGAGACTCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCCTCTGTAGATCTCTTGGCTCTCTGTGAGGATTCCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCCTCTGTAGATCTCTTGGCTCTCTGTGAGGATTCCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAAA CTGTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACATATACAAATTGGTCATCAACTGAACCTTGCCTCCAATATATTCTATACAACTT AACATTATTGAACCTTAAACCTGTACACTGTGTTTGGCTTTAAATAATAGACAATGATTTTG TCTATTACTTAGTAGACAAAGTACTTGTAGACAAAGTACTTGTGTTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAAATTTATAACAGGCCCTCTGAGCTACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTGGCTGTGCTTGCCTACAAAGCCCTTCTAT TTCATACCAATACCTTCTATTTCATAACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAACAACTTTGTTAGGAAAAAATAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGAAATGACCCCTTGGGCTCCTTTATTTGTTCTTTCAACAGGACC CCACAGATATTGCGGTATGTCATGAGGACTGGGATGCTCTTATGCTGCTGCTCTTCTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAGAGCTCAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTTATTTAAGAGAAATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATGATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCCTTACAGTACATTACCTCAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAACTGCTTAGGGTGTCTCCCAAGAGAGAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGACACTTGTCTGCTTACGGACCTCCCAAGAGTGTGACAGTTCTAT ATAGGATGCTGGATTAGTCTCTTGTATTTGTAAATAATCCCAAGAGCCGCATATGAATCTGCC

X57830	106	G C C T	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC	A	GTGGCAACTGTGGAAAGGCACACTGAGCAAGTTTTTACCTATCTGGAAGAAAAAATATGAGATTGGA AAAAATTAGACAAAGTCTAGTGGAAACCAACGATCATATCTG/CJTATGCCTCATTTTATCTGTCAAT GAAAGCGGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC	TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTATG GATCT/GJGATAAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTGTCTATACACAATTCATCTTTCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T ---			---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACCAAG/CJTJAGAGCTTCTTCCCAGAGGG CCTTTAGGATAGGAGAAAGGGTTTCATGCACACACGTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTGGCACTAGGAAGTTTCTGAGGCTGGCTGTAAGTAAAGTAAAGTAAAGG TCCA
D28513b	133	A G ---			---	ATGACCAAGCCACCACTTTAGAACCTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCAGCTCC CGCCCCCAGAGGGTCAGCACCTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGCJAV GJTGCGGTGCAAGCATGAACCTTGTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G ---			---	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAAJ/GJTTCTCCAAGTATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G ---			---	CCACTCCATCCTGATGCCCCA/JGJTTATCCACAGCCTCCTTCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCCTCAACTGATCCTACCTCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A ---			---	CTCCCTGCCCTCCTCCTGCTGCTGATGCTCGCTCTCAACAGCCGAAACCTGCTTGCATGGGGG GAGGGGCGTTTC/GJCTTCCCTTCTCTTGGCTTCTCTTATCTTCCACAACCAATCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGCTCCTCACTCCTGCTGCTGCTGGCTTTT CTGGA
D37931	64	T C ---			---	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAATGCAATTTGAGCTGTC/J CCCAGGCTCTGCTCCTCAGCTCATTTCCCTACTCTTTTCTCTATATACTCATTTCTTAAATACATT GCACCAAGAGATATGGAGACATAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAATAAGCTTCC TTT

D63807	101 C T ---	---	---	CAGGCAGGACCTCAGTGTGATGCCCTGCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCTGTTCAC/C/TAAGAGGAGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTCTGTTCCCTCCCGCTCGGCTTCGGTCTGGGAGGGTGACCTGTCCAGATGAC
D90145	21 T C ---	---	---	TGGGAACATGCGTGTGACCTC/C/JACAGCTACCTCTCTATGGACTGTTATTGCCAAACAGCCACA CTGTGGGACTCTCTTAACCTAAATTTTAAATTTATATACTATTAGTTTTTATAATTTTATTTTGAT TTCACAGTGTGTTTGTGATTTGCTCTGAGAGTTCCCTGTCCTCCACCTTCCCTCAGAGTGTG TCTGGTG
EST14035 1a	59 T C ---	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTGTTAAGTACTTCTTATTATGAGCCCCCT/C/JGAGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAT
EST16668 5	71 C T ---	---	---	GCATTTTAAATTCACATTGAATCATTATTACTATTTATGATGTTTACATAACAATTCAGTATCAT ATG/C/TTGTAGATTTCAGATGTAGGTGCTCAATACTGAGCACTTATCT
EST16904 7	57 C T ---	---	---	ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATAATTAACA/C/TTGAGATA TTCACACTTTATTATAAATAGGGTTGTGTAAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863 9	49 A G ---	---	---	TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAACTGATACACC/C/G/TTACTACTTACTC TTCACCTCTTCAAACTGATCCCTAAAGACTTCTACTTAGCAAA
EST21885 6	80 G A ---	---	---	GGCTGAAGTAGAATCAAGGTTAAGAACATTTTATGCACCTTATTCACAAACATTTACTGAGCATA CTAGGTGCTGGGA/G/TTGTGACAGTGAGCAAAAACACAA
EST22623 8a	26 A G ---	---	---	ATTTAGTGCAAAATGACAAAAGCCAA/C/G/JAGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCATATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644 2	98 A G ---	---	---	AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/C/G/JAAATGTGAAAGATGGCTTTTAAACCC
EST23587 1	31 T A ---	---	---	CCTCATTTATTTAAAGACGGACATAAAAATTTATATACAACAAAAACCCCAAGTCACATTTTCAG GAGTAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106 T C ---	---	---	AAAGATCTGGCATTATTCACATCATCTAAATATTTTGTAAATTTTCCATTTTCCATGAGTATTTTTC TGTCCAAGCATTTTAACTATCATTTTAGCGTAAATACC/C/J/GAATAACCCATAGTTACAGAAATGG GTCTGTGTAACCTCAAT
EST24308 3	45 A G ---	---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/C/G/CATTTAAAAATGTATCAAT GCACCTCTCTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73 G A ---	---	---	CTTGAACCTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATCGATTACAGGCATAAG CAGCC/C/G/J/GCCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25 T C ---	---	---	TATTGTGCATTATCAAAATGGTTA/C/JAGTTTTCAATTTAAACTGTAATGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTCGTTAGTTAATGCTACATT

EST25476 9	33 G A ---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTAAAAACCAACACA AGAGGTCCTCTGCTGCCCTTCCATGGACTGTGGCGGCTGGGACTGGACCGTGGCTGA
EST26183 2	70 T A ---	---	AGATAATGCATTAGAGCCTGCCCTCAATTGTATCTTGATTAACCTTTGTAAGATTGATCTCTAAATAAG ATT[A]ACATTCTGGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---	---	AGAAAATAAGTGCTACCAAGAACTCATGT[C]GATAGCGCTTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAAATCACACACACTGTGCCCTTAACAACAACACCGGTGACTCTGA
EST27816 5a	26 T C ---	---	CAACTCAAGGTACAAGACAATTGCATT[C]TTAACATTGTTATAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 A T ---	---	GTTTAATTGGCGTATGGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGGGGGAT
EST30226 5	25 A C ---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAAATTAGCTATCTACTGCATACATACTTCAATTGATG AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 C G ---	---	AGCTATGGTAGAGCAAAATTCACGTGGTGGTAAATCAAGAACTCTAAAGTTCAAGTAGAGAC[G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTGTGAGG
EST32515 7	25 G A ---	---	CCGAATATAAGGAAAAAATGGTGG[G/A]TGCCCTCTAAAACTGTGTAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCTCTATGAATCTGGCACTGTTTATTTTCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	TGCTTTGTTTCCCTCCAAATCCTAAAAT[C]GTGTGTCTTCAAGAAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTACCATATTCAAGTATTCTTGAATACAGGTTTCAGATACTATGGAGATGATACCATT GGACTAGGTA
EST33352 7b	75 C G ---	---	TACACATTATTCAAGAGACCACCTGACATGCATCTCCTCCGAGAAATACATTGTCCTCTCTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTTACTAAGAGAAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---	---	ATTTTCCCACAGCAGAAAGTATTTTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTCAAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTGAATCCTCTT
EST33488 7	90 A G ---	---	CCTTTGGGGAGTTTAAAGCCAGAAATGTGACAAAGTCACTTACAGGAAGACTGGGAATGTAGCCATAG TTGAATCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATCTAAGCT GCTC
EST33508 1b	45 C T ---	---	AAAAACATGCTATTGAACAAACTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCAAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---	---	---	AAAAACATGCTATTTGAACAAACATTTTATAAAGAG/GJTAAGTTGACTGAAAAAGCAGTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	---	ACAACATAGGACTGGTATTCTGGTTTGAAAAAATTATGTTGCCACTTCCTATTGTTTAAAAATGA TCATTTAAAC/C/TCTTTGAACACAGCCTGAATCCCCC
EST34739 3	97 T A ---	---	---	GAAATATCCTTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGGGGAACTCT/T/AGGTGCCTTACAACCTCAACTGCGAAGAAATTCCT TGTTGCGCTCATAAACA
EST34792 6b	104 A G ---	---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCCACTATCAATA CTCATAAGCTAATTTATCCTCAGGATGTTCCCTGA/G/GTATT CAGGAATTCCTAGTCTATTACA
EST34835 9b	93 T G ---	---	---	AAGATTTTGTGCTGTG GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGG/T/GGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATG/T/GA/TGCTTTCTGGTGGCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T --	---	---	CACAAAGGTCCACTTTACTACATGAAGGAACATAAAGGATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTG/T/GCCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	---	TCCTTTCAAATTTTGTAGTGAGCAATTAATG/C/TJATAAATTCCTGCTTAGGAATGATCTGCT ATATCTCAGAAGTTGGGCATGTTGTTTCCATTTTACTAGTTCAGAACITTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	---	CTGCCCAAATTAACITTTAGGCAAAATGGAAC/C/JAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---	---	---	ATCCAGTGCAGAGTTGAGCTGGAGACATATTTCAACCCACAAAAGGCTCCA/C/GJATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	---	TGGTCCATTATTTAAACTGAGGGAACAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCTCCCATGAAACCAAG/C/A/CTTGCTCTCATGATAAAGTGGAGACAAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---	---	---	CACCTGTTTCATTTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCTCAGCCTACAGC AGTCAGAGGAGGAGCCATGCCCCCTG/C/TGCTGATGGAGCTTGTAATTTAGCCCCAACTGATCTCA GAAAGAGGTACAAACA
EST36519 0a	33 G T ---	---	---	GCCATCAGCCCCACAAGACATGACTACCAACGC/G/TGGCCCCCTTGACCCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTCTCTGT CACAGGGTCTTAGTGT

EST36620 6	50 G A ---	---	GACTTTATTAGATAAGGGTTTGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAAGG AAGGCTTATTAAATATGGGAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	CCTGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCAGCTATGTCAGGA AAGGAAGTCTGGGATTCTTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGCTGGCCGATGATTGGAGCTTGAATAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGTCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAATTTGAGGGGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGTGATGCAGTTT[C/G]GTTA GGGAATTAAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTACTCTCTGCCAGGACGTTTGAACTCCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGCTACGGGCCGTTGGGATGTTAAAAATTGGGATTTTAAATTAAGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTTGAAGTCT[T/G]CAGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACCTCTAGGA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGCTCTGTAGCTTGTCTGGGCTGAACCTAAAGATATCCTCCTGCTCAGCCTCCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCAAACACATTTTTTCAAGGCACCTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---	---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAATAACCTCAATTCTGTAAGAACTT/G JAACATGCTCAAAAAAGAGGGGAAAAAACTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---	---	---	AAGACATAAATCTGCAATGAATCAGTTATGAAATATTAAACCTCT/GA/CJTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACACCTTAAATCAATGACGTAGAA
EST37613 6	34 A G ---	---	---	CTAGGCATGGGGCTTTACAGTCATTTATTACG/A/GJGTCATGAATTCATTAACAAACACAGCGAT ATAGCAATGAGCAAAACAGACCTCCCCAAAATCACCTCGGTTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---	---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTA/T/GJTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCGCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---	---	---	TCTACAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA/C/TJCGCATGG AAGAAGCTCTCCTTTAATTCCTAATCTCTCTCTGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---	---	---	TAAATCAAGGCTCTTTTATTACCAAAACAAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGCATCCTGACTGAQ/T/CJGTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---	---	---	TTTATTGCAAAAGTAAGCAGCCGGT/CJTGTCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---	---	---	TTTTTTGTTACTCTGTAGCCAGTCATTAAATCTGAAGGTTTAAATATATCATTTTATTGGGATGAGATCA TAGCTTTACACAATGCTATG/T/CJAAACAAGTTACTGAATATTTTACCTCGTGGAGTTG
EST39331 1	70 G C ---	---	---	TCCTCTTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TGC/GCJGTGTTTAGGGAGAGCTGGCAGCTGGCCCTAATCTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---	---	---	GTACGATTGACCTTACATAGTGCCTCTAGT/C/AJACCTATGAGGCACTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---	---	---	TTCTAATAGCATGCCCTGTGACAGGGAACCTAAGCTC/T/CJTCAAAATAACTGAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42 A G ---	---	---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA/GJATAAAGTCACATCAAGACTAA TAATCTAAATGTAGTTTGTACACCATTTCTCATTGAACTAGTCCCTGCAAGACACCTTCTA CCCTGCACTTTTGGGGAG
EST40579 1	81 A C ---	---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCTTCTTACCTAAAGTGTGTCTATCTG AGCTGGTGGAAA/A/CJGGACTTGGAGACAGCGATTAAATACGGAACAAGGCTTCCAGGAAG
EST40584 3	68 A G ---	---	---	TTGTATGGTTGAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A/AJGTCTGTACTCCCAATAATCTCTAATGTTTAAAGCT

EST51340	51 G A ---		---		GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---		---		CATGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA TTCJTTTCCCTTGGTCTCCAGTGGAGGGGAAAGCCCATGATCTTCAAGCAGGGGAAAGCCCAAGTGAGT AGCTG
K01506	63 T C ---		---		CTGAACCTCCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTCTCAGTTCATGTGAAACACTAT/CJC CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAGCAGTCATTCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
L18877	69 T C ---		---		TGAGTCTGAGCAGAGTTGCAGCCAGGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC C/T/CJATCCATTAGTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTCTGTCTATTGGATGACTTTGAGATTATCTTTGTTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---		---		GCTATTTTACATATCCCAAGCCCTTAGGGCTACAGT/CJC/TCTTGTCTGTGACCCCTGTAGGGTGCCA TTTGAGTTTACAGCCTAGAAGAAAGAAAGGCTTTGGGCCCTGGTGTGGTGCATAGGCCCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAACCTGGGCAAT GT
L38517	137 G C ---		---		GGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACCCAGCGTCCCCAC CC/GCJCGTGTGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---		---		ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGGCACTGTGATGATGAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGGACAGGGCAACAAAATACAGTAGTATTTCTTTTGTATTTGTATATT/GJCGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCGGTGGGCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---		---		CAAAGTTGTCTCTGCCCATGAGCACCACAGTCAGGCCCTTGAGGGGATCTCTAGGGAGACAACAGC CCTGTCTCAAACCTGGTTGCCAGTCCAATGTACCAGCAGCTGGAATCTGAAGCCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACACCCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 T C ---				AAGTGAACAGAAAGCAAGATGGATTGTGTTCTCTATATAAAGCACATAGTATGTTTACTGGTATCGT AAGAAAGCTGGAAGAGAGCTCAAGTTTTTGTTTACTTTTCAGAAATTCGAAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---				GCGCACAGTCCAAAATACAAATGGACAGAAGATCTATATTGTACCAGAAGT[G/A]TTTTATTTCACC CCATCAAGTATAAGGTTACTGATTGATTGGTCTTTTATAAACATTTGGTATATTCCATTTCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113 T C ---				TAGGATCTGTGCCAGGCCATTGACACAGCCAGCCACCCACTCCACCCCTGTAGTGTCCACCCCC TGGACTGGTGGCCCCCACCCTGCGGGAGGCTCCCATGTGCCGTTCGCGCAAGAGACAGACAGAG AAGGCTGCAGAGTCTCTTTGTTGCTCAGCAGGGGCTCCGCCCTCCCTCTCTCGCTTCTAATA GC
M21539	114 T G ---				TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATATCCCGACAGCAAAATTCGTTTCTCTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCTTTTCAGAGCT TCTCTTGGGTCG
M26041c	173 A G ---				CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCTGACTTC CTGATTTTTTCTTTCTCA/GTGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---				CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCTGACTTC CTGATTTTTTCTTTCTCA/GTGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---				CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCTGACTTC TCTCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATATTTCCTGACTTC TCTCTGATTTTTTCTTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M53967	57 G C ---				TAAGGCAGCTGTACGGGAGGCCAGTCCAGTCCAGCAATTCACAACCCACTTTCAGTGTGCTGCT TGCCAAAGCTGTTTTAAAGCCCAAGAACACCTTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---				ACTTACTACCTCACCTGTACGGCTGACGGGA[G/A]GAACCACTGCACCAACCCGAGAGAGGCTGGG ATGGGCTGCTCTCTGCTTTGGGAGAAACGCTTGTCTGGGAGGGGCTTGTCTGTCAAGGTTCT CAACTGGAAACCTTAGGACAGGGTCCCTGCTGTGTCTCCCAAAAGGACTTGACTTGCATTTCTAACC T

U06641d	166	C T	---			CTCCTCCCTTATTTTCAGCATGGAGGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAATTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAAATTT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]GGAAATATTCTATGTCATGATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39	T C	---			GAGGCTTATGAGGTCCTCTACTCAGGAACACCCCAAT/CJGACATTGCAATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTAAGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTGTAGTCTCTGGCCCAAGAAAGCAAGAACCAAAATTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C	---			GAGCAGAAAGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCAAAAGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C/T]ACATCTGCCCGCCCTTCCAGCCCTTCCCGAGCCCTCTCTTGTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	C G	---			GTGACATGAGGCCCCATT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTCTGGGTTCCCTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTTAAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C	---			AAAAAGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCAAAAGTTGTTTAAAC CTCTTTGTTTCAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAAAGAGAT[C/T]TACCCTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	T C	---			TTTCTGTCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAGAAATTAATAGCAATGCTGAACATCAGGAATGTAGATATCCGTACAGAGAGT TCCAGTAAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C/T]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	T C	---			TCCAATTATTGTCCCAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACTCCACGGGATTAAACAGAACGTCCTTGCAGACTGAGCGATGACACCACAT[C/T]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTCTGGGAAAACAACACTGCTCTTGG AATTA
U18543	58	T C	---			GCACATGCAGAAATAGACTCAGCCTATGTCCTGATCCAGCTGGGTAGTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTTATTGTTATGTCCCTCCCGGCTCCACCTAAATTTAGAGCTTTAAA AGATGCACCTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGTAGTAAATAGGCACCTCC AAGGCTTTAGTAGAGAGGCC

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U25975b	164 C A ---	---	---	<p>TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAATTAIT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAGAAATTTGCAAAAAGAC[A/A]AGATGACTTTTATATGAACCCCTCTTTAGG GTCCAGAAGGAATTGTGGACTGA</p>
U25975a	143 C G ---	---	---	<p>TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAATTAIT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAGAAATTTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTCTTTAGG GTCCAGAAGGAATTGTGGACTGA</p>
U25997	61 A G ---	---	---	<p>CAGGGAGAGGTTATTCAACCCCTCACCAACTAGTATCATTTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTTGATTTTAAAGTAGTCTCTATTTCTATCCCTTTAAAGAAAATTT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTTCTGCAATGGCAGCATTCGCCACCAACAAA TCC</p>
U28413	29 C T ---	---	---	<p>ATTCCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCCCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCTTGATCC CAGATGTTGTGGCCTGGGAAGCCCTCATTGCTACAGTACAAGTAAACACAAGTCGTTGTACCTCAGTT G</p>
U30884c	89 A G ---	---	---	<p>TAGGGGTAGCATTAAAGATTCAAGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATTTCCACGTTAGCC[A/G]TTGTTCTTTGATGAATCTATATGAGTCATAGAACACAAAATCTAT TGACGGAAGTCATTAGAAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACACAGTTGAACACAAAGT GCTGTCA</p>
U30884a	34 A G ---	---	---	<p>TAGGGGTAGCATTAAAGATTCAAGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAAATTTCTTGATGAATCTATATGAGTCATAGAACACAAAATCTAT TGACGGAAGTCATTAGAAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACACAGTTGAACACAAAGT GCTGTCA</p>
U31216b	78 A G ---	---	---	<p>GGGACAGCATATGTGGACCCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTATCA[A/G]CCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCTTTACAACGTAGAGGAGGAGGATGCCACGCCGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT</p>
U31216a	70 G A ---	---	---	<p>GGGACAGCATATGTGGACCCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC[G/A]TCATCAAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCTTTACAACGTAGAGGAGGAGGATGCCACGCCGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT</p>

U31416c	76 G A ---	---	AGTTGCCAGCTCCCATGTACAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTGCTTACAAATGCTAGGTCCCACTGCCTGCT GGAAAGAAACACACACTCCTTTGCTTAGCCCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---	---	AGTTGCCAGCTCCCATGTACAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCCTCTCTCTGCTTACAAATGCTAGGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---	---	ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCCCTCC AGACCGCAGG[C/T]TCCCCCAGCCTCAGGTTGCTGGAGCTGCACATGACTGCATCCTGCCTGCCAGG GCTGCAAAGCAAGGCTTCTCTATCTGGGGGACGCTGCTCGAGAGAGGCGCGAGAGCGCGCAGAAC ATGCCAGGTGTCC
U37690	54 A G ---	---	GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT/GJCCCCGAAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCCTGGCCGAGTGCTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---	---	TGAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]JACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTCTCTCTATAACCCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---	---	TCAAGAAGGTGACTGCCCTTGATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTAGCCTCTCTGAGACCATGTGGTTTTAAAA[AT]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCTAGAATTTGGATTCTCTCTGTTTTTTCATGCTCTCTCTT GTAACCTGAGATCATCAG
X52011b	148 C T ---	---	AGGAAGATCCCACCGACCTTCTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAACATTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAAGAAAGTTGCGAAAATTGCG AAATCTGTTGTGCA[C/T]GCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A C ---	---	AGGAAGATCCCACCGACCTTCTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAACATTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAAGAA[AT]GTTGCGAAAATT GCGAAATCTGTTGTGACGCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGCTTCTCTCCAC[AG]TGACACAGCTTCCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCCAGGGCCTCCAGGACTGGGCTTGCCAGGCTTGCCAGGCTTGCAAAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCAGGGCCTGGCCTTGTCOCACGCCACCTGGCCCCCTTCTTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTAATTTGCTCT[AG]ATACAAAATTC TAAATCAATATTGAAATAG GATGCACACAATTTACTAAAGTACAGACATCCTAGCATTTTGTCGGGCTCATTTTGCTCAACATGGTA GCCGTGCTCAGACACCTCCAGAACGCGAGGTGCTGGGCGCCGTTCTGCCGGACCCCGGGAACCTCTC CTGCCGGAAGCGGACGGCAGGGATGGGCCCCAACTTCGCCCTGCCACTTGACTTCAACAAATCCCT TCCTGGAGACTTG[AA]AACCTGGTCTCAGGAGCGAAGGACTGTGAACTTGTGGCCTGAAGAGCCAGA GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTACACTTGATTGTATATAAGATAA[IT/G]T CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAAACATTAAATTAATTTCTCATACCTTA TTGCACAGGAAGCATTTATACTTGAGAAAAATTTGTATAAAGATGGAAAAAGTCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X66924	147 G A ---	---	CTCAACCCATAACCTCAACACACATCT[CT]ATCCTCCACCCACATCCACACATCCACCTCCATCC CCAACCCATCTCATCCCAACTACAGCCCCCAACCCAGCCCCAGACTAATCCACAGCCATCCCAA CTCATCTCATCCCAACTGCAGCCCCAAACCCCAACCCAGGGCATCCCCAACCCATCCCCCAAGCC AAACTCAACACCATCC
X78932	62 T G ---	---	ACCCCAACTCAAGTCCAGGCCCGCCAGGCATCTTCTGCCCTGCCCTTGCTTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTCTAGCTACTTCTCTG[C]CAGCTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG ACCCCAACTCAAGTCCAGGCCCGCCAGGC[AG]TCTTCTGCCCTGCCCTTGCTTGGCCCATCCAGTCC AGGGGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG GGACCCAGAGTGACCAAGTCCAGGAGGGCGGCGCCCTCGCCGTGTCGGTGTCTTTCTTTT CAGCCCCGAGAGGTCCTGACCTGGGGCTTCTCCAGGCTCTGCGCCACGCTCCCGCCCGCTCT CTTTCTCCCAAGC[GA]AAACCAATGCGCCCTTCACTTGGCTGCCGTGCCAGGGCGGGGGCTT CTTTCAGAGC
X80026	25 T C ---	---	ACCCAGCCAGTGTCTAAGGACATGGATCGGGTGCCCGCCAGACGTGTGCACAGGGGACCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT[GGGGC ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA
X80197b	99 G C ---	---	
X80197a	28 A G ---	---	
X85106	150 G A ---	---	
X87160	128 T G ---	---	

X87344	34 C T ---		CATCCCAAGGCACTGGTGTGACTCTGCTCCTGTCG/CMACTGACCAGAGACCTCTGCCTGTGCACTGC AAGCTGTGTCTACTCAGGCCCAAGGGGACTCTCTGTTTCCATTCTCCCCACAGACCTGTCAAGAG AAGCATGACAACAAAATCAITTTACCGACTTTTAGTGCTTTTTT
X87838	179 G T ---		GGTGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCTATGGGAACAATTGA AGTAACCTTTTGTCTGGTCTTTTGGTCGAGGAGTAACAATACAAATGAGATTTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAATGGATCACAAAGATGGAATTTA/G/TCAAACCCCTAGCCCTTGCTT GTAAAAAT
Z14138	81 A G ---		GTTCTGCTGCCCTACACAGGGGCCCTGTACAGTGAATGGTGCAATTTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC[A/G]TGAATGTGCCCTCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACACAGGTCTCAAGGTTCTCAITTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191 A C ---		TAACTCTCACCATTCTCAGGTATAAGTTCTATAAACAGGCTTGGAACTCTGGGTAATTAATAAACACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTTCATACAGTTCTTTTCAAAGTGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTTC CAGTACTGGTTTTCCAA
Z23091	159 G A ---		AGAACCTGACCAGTGTGGCTCGGAGGGGAATCCAGACCCGCTGCTGTCTTGTCTGCCCTCCCCTCCC CACTCCTCCTCTCTTCTCTCTCTCTCACTGCGACGCCCTCCCTTCCCTCCTCCTCCCCTCCTCGG CTCTGTGCTCTTCAITCTCA[G/A]GGCCCGCAACCCCTCCTCTCTGTCCCGCCGCTCTCTGGA CTGAGCTTGACGTTTG
11595b	125 A G ---		GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAACCTGACCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTACCTTGTCTTTGTGTTGAAGGAGTGTTTCCCATGACTGTTTAAAGTGACAAGTGCCATGG ATATCTACACCGTCACAGACTAGATTGTCTCAATGTCCTTGGCTTGGCAG
11595	125 A G ---		GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTTCTGCAAGGGCAGGTTTGAACCTGACCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTACCTTGTCTTTGTGTTGAAGGAGTGTTTCCCATGACTGTTTAAAGTGACAAGTGCCATGG ATATCTACACCGTCACAGACTAGATTGTCTCAATGTCCTTGGCTTGGCAG
1241	131 G T ---		TATATCACATTAGTATGTCACCTGCCATGGTAAGGACTTTTATCAGTAGGAAATAGAACACTTTTGAA TGGTCTTGTCCCTTCAATAAAAGAGTGACATGATTGAACATGTGTTTTAGATAAAGGGCACTT[GT JGCAAGGAGTGTTAGGATGAAGAGAGAAGAGATTAAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAAATAGGAGGCCCTGAGATCCACTGGATAATCTATAAAAAACCAAGAGAAAAG

1282	130	C T ---	---	GTGCGATCACCACCTACAGTCTAAATTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTGACCCATTAGCAAATTTCTCTCATTCTGCCCTCACCCCCAGGCCCTACTCTTTATCGCTATAGATTTGCCIC/TACTTGACATATCATACACATGGAGCCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACTGAGAATAATGTTTTCAAGGT
6810	68	C T ---	---	AGTATCACACATCTTAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACITTTA/C/TAAGAGCATTTTTTAAATTTACAACACAAAGCTCAACGAACCTACAATAAGICTAGTAGTCTGTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTTAAAATGTCTATGAACAAGTACAAATTTCTTTTGGTCTCGAGAGCAATGACCCTAAGAAATATTTTTAAAGGC
6817	118	A C ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC/A/C/JGTGGATACCCCTG TGTGCTCTACTGGCTCCAAAGGCATTGAGGGGATCATCAAGAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAAGTGGCGGCTGTGCAGATCGGCTTTTGGTTGGTGTCTTAG
6819b	212	C ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACCGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166	G T ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACCGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTT[G/TA/TATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39	A G ---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[G/TTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149	G T ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTGGTAAAGTAACTATTGATTATG CACAATTTCAAG/GT/CCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A G ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTGGTAAAGTAAAGTAACTATTGATT TGGCCACAATTTCAAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGIGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTG[A/G]GATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTA[C/T]CAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC TCAATGAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCTCGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGAC[A/C]GJCAAAGCCAAAGGAAC TCAATGAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCTCGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---			AAAGGTAATCAAAAGTCCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCTCGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTAGTCTATCTTCAAGGTCCCAATA[A/T]CCTTGAGGTTCCCT
7998b	94 A C ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTTTAATGAATGGGTAGTCT[A/C]TCTCAAGGTCCCAATAACCTTGAGGTTCCCT
7998a	75 A T ---			GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCCTATTTCAGACATCTTGCAGCTCTCCTGTA ATACTT[A/T]ATGAATGGGTAGTCTTCTCAAGGTCCCAATAACCTTGAGGTTCCCT
8071	119 A G ---			AAATACAGAAATTTTATTAGAACTGTTTAAAGTAGAAAAAACCCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAATGGAATTTTAGGGCAACAAAAGTCTAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAAATCCACACAGAGCATGCCTACACACATTTTATCAT
8467b	93 C T ---			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATTTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTA[A/C]TGGTCACTCCGAACCTCCTTCAGAGAGCAAGCAAAAA TTAAGTGTGATACTGGAGCTTATGTCATGCAAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8467a	70 A G ---			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATTTTGGCTTATCATT TG[A/G]CGCAAAATCCACTTTGCTGTAACCGTCACTCCGAACCTCCTTCAGAGAGCAAGCAAAAA TTAAGTGTGATACTGGAGCTTATGTCATGCAAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8498	84 C T ---			AGGGTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACCTTCAATTAATCGAAAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCTCAATACAGAACCCAGGAATGTAATTTTCCCTAACTCAG

WI-18562	29	G A ---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTGTAACCCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---			TAAGCTGTTCCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G A ---			GACTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCCTTCCTCGTGAGAC
WI-18563	94	A G ---			AAATAAGTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---			GTCTATTTCATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTATTATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A ---			AACTTTATTGTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGTTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71	T C ---			AACTTTATTGTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGT[C/A]AACAGGTACATAGGTAAACCAAAGTATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	A G ---			AACTTTATTGTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18619	44	G A ---			TTTATTACAATATTAGGTGGCACAACTAACTAACAGCTTCTGA[G/A]ACAGGAGGTAACATTTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76	G A ---			TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAAATAA TGGAGCTACAACCCACCC
WI-18535	107	G A ---			GTAATAAAGTTTATTGGCACAGCCACGCTCGTTTCATTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCGGTG
D17525	107	C T ---			AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTACTAGTTTTCAGTTCTGGGCAGGTGAC TTCATCTCTCGAACTTCAGTTTCTTCATAAGATGGAAC[G/T]GCTATACCTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACCTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAGGTGATGTCTACACGGCAGACGAAG

DWU-133c	313 A G ---	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C ---	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T ---	---	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC TTCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTTGTGTGGGCACCTCCTACGTCACAAATGAAGTG TGTTTCCCTTCAGTGCATCTGGGAAGATTTCTACCCCTTGACCAACAGTTCCTCAGCTTCCATTCGCC CCTCATTTATCCCTCAACCCAGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTCATGTGGAATATAAAGAT
DWU-387	169 G T ---	---	GTGTATAAAATGCAACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACCTGCCAACAAGTTCACCTCATATATAAGCAATATTTTAA CTCTTTTGAGGTGAATATAATTTATATTACAATG[G/T]AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAAAGTAATAACACAAATGAAGTGTATTATTCAA
DWU-447b	172 --- --- ---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTGAATAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTTGTCTAAGAGGATTGANAATCAGTTTAGTTAAATGCTTTCTGTAG GCCCTTCTTCTTACAATGAAGAGATGATTTCTCTAGTTTATGGTTA
DWU-447	85 A G ---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAAGTACACTGTAATTAATTAGTTTGAATAGAGCACAAGCTTAGCTAAT CAACCATATTTTCAATTTTGTCTAAGAGGATTGANAATCAGTTTAGTTAAATGCTTTCTGTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTTCTCTAGTTTATGGTTA
DWU-476	63 C G ---	---	GTAAATTCAGTTTTTTCCAGTTCTCTTTTGTGCTGCTTCTCAATAGCGTTTAAAGGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTTT

DWU-505	67 A T ---	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTCCCCATACAGAAAAATCTATCACCATACAAAAATTTA A/TJTGCAAGTATTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAAGTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	---	AAAAATCCAGGCAATTCGAATCTGTTTTTTCATGATTTATAGAGGTTTACACAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAAGGTGAACCTGCTTTTGAATATCCAGATGTTTGGTC A/GJ TGCATGATGCGAGTGAGCAGGTATGTTGTTGCTTTGCTTGCACTGAAATTAATTTGCTATCAAGAGC AAACTATGAACGGTTTTTTTATTCAGATGTCCTCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATCTTTTCAGCTTGTTCCTATACCTGTTTGT ATATACAGTTTTTGTAAACCATATGATTGA A/CJAAGAAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTTGTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATTTCTAGTCTCTGATTTCG
DWU-59	94 C T ---	---	---	CATTTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAACATGCTGAGAAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTACATTGGC C/TJGAGCCGTGTTTCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAGTGGTTTTACTTCTGATAGCCGGTATTTCCCTCCTAGCAGACATG CCACACCGGGTAAGAGCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGGTGAATTTTGTGTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCTTCGCCTGCATTGCAAGAGGAGAGCCAGGTCCTCCTGGAGAA C/TJG CTGGTTCCCAAGCCCAACACCCGGCTTTTGACCCACACAGGCTGTTGAGGCAGGAGGTGGTGAAGACGT AGCTGTAGACCCCAAGCAACCCAGCCCTGGACCCCTGGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGTCATCCCATCATTTAGACAAGACACATCCTACATAATAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTACATTTGGTGGCATTTGTTGAATAGCTACAGAA A/GJGAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTCATAATCTGACAGGTCAAGTAAAGTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18035a	27 T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT T/CJAAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTCATAATCTGACAGGTCAAGTAAAGTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCTTAACTGCTAACTTTTCACTTACTGAGATTATTTTCAGGCCAAT GTGTC TJTGTTGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTTCTGTTTCA

WI-18063	105	GA	---			AGGCTTTAAACTGATAACAAATTTGCCCTTTAATCACATACAAAACCTCTGCACCTTTTCATCTCCTTC
					---	CCATGTTTTCTGATTTGATGTAACCTTAAATTTGTGATCCCTTTAAACAATATACGTAGCTGCA
WI-18078	86	AT	---			AGTTGAAAGATCAGAGAGTTATGGTTGGTAGTAGCTGAACCTCAGATTCAAACCTGGTCCAGTGTG
					---	TTGTTTTTTCAGCATCAGATGTGCCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	TC	---			CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTTCATCCTTTTGTAAATCCATCAGACACTGTGGT
					---	TTTCATCTCTAGAAGTTTGACCTTTCGGCCCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38	TC	---			GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGATTCJTTGTAATGGATTGGAGTACTTAC
					---	CACATTTTCATCTGCTCTGAAATAGTTCACTAACCAACTACTGACAACAGTTTAAATTTGGTTCTT
WI-18142	66	TG	---			TTCAAGATAATTACAAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAATAATCTATATACI
					---	T/GJCCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18178	68	TC	---			GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCACTCCATGCCTGGAGGTTAGTCTGGGG
					---	GT/CJCGCGGGATGGACACACAGACAGACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	GT	---			TCAATCTGAAAACCTTGCTGAAGCCAGCATGGGGTGGTGGGAGGTGATTATGGCTGGGGAAGATG
					---	GGCACTCACCGACAGCAGCATCTAGCACACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	GA	---			ACAGATGTCAGTTGTTGAATTGGCCCATTAAGTATGGGCTTTCTTGTAAAAAGTCAATCCAAA
					---	AGGCTTGGCAAGAGTTTGTCTATACAACGGAGGACAGAGAAACATGA/GJCTGGGGAGTAGGCTCT
WI-18261	26	GA	---			GACAGAAGGTGGGCTGTC
					---	GATTTGAAGGGATTGCTTTATTAACTGATGAAAGCGTGATAGAGGAACTGTTTAAAGATAACAA
WI-18268	88	CT	---			CTTATAAATACTCCCAATTGTAGAAGTGAAAGATTG
					---	TAGAGGGGAAAAGGAGGTGGGCTGCCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC
					---	TTCTTACTTCCCCCATAGATTC/JCCTGACAATGTGCTGCAGAACCTCCAACTGGAAAC
WI-18299f	107	CA	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCAATTAACCTGGTTGCCAATTTTT
					---	ATCTATTTGGGTCTGAGAAATCCACAATTTTGA/GJGAATCTTTTGCCAAATTTTGACATATCTG
WI-18299e	101	AG	---			CAG
					---	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCAATTAACCTGGTTGCCAATTTTT
WI-18299d	77	GA	---			ATCTATTTG/GJGTCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAAATTTTGACATATCTG
					---	CAG
WI-18299c	67	TG	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCAATTAACCTGGTTGCCAATTTTT
					---	T/GJATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAAATTTTGACATATCTG
					---	CAG

WI-18299b	52	G A ---				TCACAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACTTG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGCCAAATATTGACATATTCTG CAG
WI-18299a	48	C T ---				TCACAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAA[C/T]TTGGTTTGCCAAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGCCAAATATTGACATATTCTG CAG
WI-18307	76	G A ---				TCAACTGTACCAAGTTTAGCAGCAAGAGGATACTTCTTAGAGACTTTCAGTGGACTTAAACTCAG TTCCGGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T ---				TTGGTATGAATCTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C ---				ATGAAGTCACTTCAATCATAGGGTCAAGAGAAAGAATGTTTTTCAGAT[C/T]TAAATCTATGAAAA GGTGTATCTGCTTGCATTTTAAAGAAACAACAAGTCA
WI-18395	77	G C ---				TC TTGACATGATCTGTGAAATAACGTGATTGTGGTTTCTCGGAAAAATTTGAAGAATAAATTG ATTATTCAG[G/C]TGTGCAATTTTAAAGAAACAACAAGTCA
WI-18398	62	G T ---				TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACCAAGGGTT[G/T] GATAACATTGCCAGTAAACCAATAATTCAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
						CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTTCGCTCTTTCTAAATTTAAAGAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18396	21	C A ---				AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTAGAGATTTTTTTTCCCTTTAATCCTTTTCAAT TCAAGGATCATCAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
WI-18409a	20	C A ---				AAAAAGGAAAAAGGATGGAGTAAGAGAGAGAGACAGAGGAAACAAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAGAGAAAAAAGG TTTTAGGTGGGAGAGAGGA
WI-18442	62	C T ---				TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCCTCATATTTTCCAACCA
WI-18452	38	G A ---				ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	A C ---				CTGGTGGGAGGAAACAAATTTGGGTATATTTCATACAATGGAAAACTCTTCAGAAAATAAGAAAGGAA CAACCACTGAATCACACAACATGGACAAATCTCAATCATTTATGCTGATGGAAAGAAACCATTCA TAAGAAATACACAGTACAT
EST5b	93	A ---				

EST5	93 A	---			CTGGTGGGAGGAAACAAATTGGTGATATTATTCATACAAATGGAAGAACTCTCAGAAATAGAAAGGAA CAAAACACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAGAAACCAATTCAT TAAGAAATACACAGTACAT
EST6	48 C	---			TTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCAATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTCTTCTTTTGCACAAAGCAAAAGCAAAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A	---			GGACAGGACCTCTATCCCGCTGTGGAGCAGCGGTGATGAGTGAAGCCAGGCCCCAGGGATACTGGGCC CTCTCTCAGGGCGTCTCAGGACCCAGAGCTGTCTCTGTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTCTTTGGTGGGT
WI- 18740c	104 G	---			TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAATCTCATTTACCATCATGTATCCAGTAGTG/GJATAATTCAATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C	---			TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAATCTCATTTACCATCATGTATC/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C	---			CCAAAGTCTCTGTTGCTCATAAAGATTTTGGGATGGGAGAGAAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCTTCTATTTACAGAGGTAGCACAA/CJTJGATTCCAACACAAAACCCCTTCCCC TTTTAAATGATTCTGTTCTTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTTCTCTT TGAAGCAATGACAAGCACCTTACTTTCACGGTGGTTTGTGTTTCTTAT
WI-18746	114 G	---			GCCAGCAGCTGAAGTCTCTTTCTCTCTCTGGCTGGAAGAACATCAAGATACTTTGCGTGGATCA AGCTTGTTGTAATGACCGTTTTTATATTACTTTTGTAAATATCTT[G/A]TCCACATCTACTTCAGCT TTGGATGGTTACCG
WI-19112	212 G	---			CCGTGTTACACACACAAATGGCAAGCATAGTCGCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGCTATCTCATGACAACCAACAGAAACCGACGACAAA TCCTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTTGAACACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTCAAAACAGTCCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A	---			TGGTGGCTGGCTAGTATTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAACACACTCTCTTCTTAGCCTTACTTTGAATCTTGCCCTATAATAAAGTAGAGCAACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTT[C/A]ATGATTAGCCGTGTAAC
WI-19057i	175 G	---			CCCATTTATTATAGGCCAGTGTCTCAAAGAGTAGAGGAGGCTCTACTGGTCTTCAACTCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGAGTCCAGGCCAGCCGACCTG TCTTCATGCGAAGAACACAGTGCCAGATCCCCACAGCTC[G/A]TCTCTCATCTTGGTTTGGCCACA

WI-20103	168 C T ---				TGGGACTTCCAACTCAGAGGATGTGGGAATCCCAGCTCAAATATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAAGCTGGGTCTCCCA/C/JTTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---				GCCTTACCCATTTGCACATATACATATGCACCACCTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA/G/JTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCTACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---				TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTTTTA/G/JACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---				GTCCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA/G/JAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156 A C ---				GTCCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAA/JC/JAGTTGGAAAAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47 A G ---				CAGTAAAGAGTGATTCAAGTTGCAGTATACACTGACAGGTAATAA/G/JTATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---				GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCAATCAGGCAATA ATTGTTTCCCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGGACTTACACATTTCAAGTTTGACAG T/C/JGAAAAACCAACTGGAGCTGCTTTTCCAAAGAAATGTTCTGTGTCCTTCAAAATAGGAATTCATG TTATTTCTTCTGGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ---				GAGTGCCATACCTTCTCCAGGCCTCTGCCCAAGAGCAGGAGGTGCCT/G/JAAGCTGGGAGCGT GGGCTCAGCAGGGCTGTACCTCCCATCCCGTAAGAOCCTCTTCCCTTCCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ---				AGCAGTGGCCTTATTGCATCCCAAAACCACGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCACC[G/JGGAAGCCG TCCTGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCAT GTCTGGGACACACAGACTATTTTAGATTTCCTTTGCTTTTGCAACC

WI-20146	31	T C	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/C/CATTTTGAGATAAAGTCAAATGCCAAACACTAGCTCTGTATTAAATCCCATCATTACTGGTAAAGCCTCATTTGAAATGTGTAATTCATACAGGC
WI-18922	74	G A	---	---	TAGGAATTGGTTTACGCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGC/G/AJCTGGCTCTAATTCACAGTGTCTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAGAGGCCACACAGTTCTC
WI-18763b	53	A G	---	---	TTTCGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/G/JATTATTAGAATGTACCATAATTTTGTAAATATTATATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38	A G	---	---	TGTGTTTTGCCAA
WI-18771b	75	G A	---	---	TTTCGTGTGTGGGGTCAACCGTACAATGGTGTGGGA/G/JTGACGATGATGTGAATATTAGAATGTACCATAATTTTGTAAATATTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771a	57	A G	---	---	TGTGTTTTGCCAA
WI-18820	70	T C	---	---	CTCATTTCCATGGCAATGTGGAAATTGAGCAGAGAACCTGCTCTGGAGGATGCCTAGAAATGTTGGGAACAGAA/G/AJAATAAACTGAGTTTAAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18742b	51	C T	---	---	CTCATTTCCATGGCAATGTGGAAATTGAGCAGAGAACCTGCTCTGGAGGATGCCTAG/A/GJAGATGTTGGGAACAGAAATAAACTGAGTTTAAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18882	94	C T	---	---	GGGAAAAATTTGAGACGCAATACCAATACCTAGGATTTGGTCTTGGTGTGATGAAATTTCTGAGGC/C/JTGATTTAAATCTTTTCATTGATGTGATTTCTTTTAGGTATATTGCGCTAAGTGAAACTTTGTCA
WI-19970b	167	G A	---	---	ACAAAGTCTGTAGCCCCCTCACCTTCTCTGTTTTCACCTTTTGCCAAATGA/C/JATCGGGTTTGGTTTCTTTGATTTAATAACGGTTGTGGTTTCTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGAGTTTACC
WI-19970a	126	T C	---	---	GTGTGTCCAAAAATGGGGTCTCTCTGCTACCTTGACCCCTTCCCTTTCCCTGCTCTCTCTCCTCATCATCATTTCCCAACAACATCCTCTGCCA/C/JACACAACAAAAACGTAAGTTTCAATTTGGGCAAAAAATTGAGC
					TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCAACCCGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCAGTGGGGGAOCAGCAAAGGCCTTCTCACTGGTTGTCAAAG/G/AJTAGTCACTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCCAGAAATCTTTAAACGACTGACCTTCTCTTAAAAACAGA
					TATAAGCCCGGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCAACCCGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCAGTGGGGGGACCAGCAAGGCTTCTCACTGGTTGGTCAAAGGTAGTCACTTGGCCTGGTGCATCCACAGAGGATGTTGTTCAAACCCAGAAATCTTTAAACGACTGACCTTCTCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCCTGCTCCCGACAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAAAT/ GACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTAATC
WI-19067c	153 G C ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCCTGCTCCCGACAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJAGAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTAATC
WI-19067b	151 T C ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCCTGCTCCCGACAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTG/CJGGAGAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTAATC
WI-19067a	57 C G ---	---	TATTGCTGCTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC/CJGCTGGCTG TGCATATCCCTCCTGCTCCCGACAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTT CTCTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTAATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCCCTGTAGTTATTTAGGAGACAGTCTCAAGCAGTCAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCAAAATAGCACATCTCCCAACGTTAAAGACAGTGGATCATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATTGTTTGGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAAAT/CJTTGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTTTACACACCTACTAAAAAGTTATTATGATGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTTACCTAGCATTTCAAAACCC AAATGGCTAGAAC/A/GTGTTTAATAATTTCACAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCATTTCTTTCTTCTTAAATAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAACTAAATTTATTATGCCCTCTTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTTA AAATAAATAAACCTTTGGGAAAGGTGTAA/G/A/CAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCAGGAACTGGAATAAGCCTTCGAAAGAAATTTGCTTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACCTGTTGCTGATTTTGACCTTGATTTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAAATACCCCTGTACATATCTTTGAGTTCAAC/CJCTTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACCTGTCTTGGGAAGACAGTCTGTGGCTTG

WI-19042	193 A C ---			TTTGTAGTGTGGCTCTCGCAATGCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG ACACAAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAATAACTTAACCA/A/CJGGCTG TGTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---			ATTGGCCCTGTACAGTTTGTCTATTATAAATCATTTAAACACACTACAGGTGTGAATGGTTAAAA TGTAAGCCCTCCAGTTCAATTTTCAGTTATTTCTGAGTGTGCAGACAGCTATTTGCACTGTATTAAT GTAACCTATTTAATGAATCAGAAGCAGTAGACAGATGTTGGTGAATACAAATATTGTGATGCATT TATCTT/A/CJATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---			GCTTCAATTGGCGATTGATTCAAGTGCCCAATGTAAACAGGGTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCTTATTGTAATCTT/AJGTAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTGGAGGCC ACAGAGGCT/CJGGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACTTCGTGTCTCAG GTGCTGTGT
WI-18821a	69 C T ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTGGAGGCC A/CJTAGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACTTCGTGTCTCAG GTGCTGTGT
WI-19021a	20 C G ---			ACTCCTCTGCTGTCCATC/GJACTGTCTTTTGAACAGGAAAGTACACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAAGTGTCTCTCCATCACGTTG CTACCTTACCCACACTCCCTCTGATTGCGTGAGGACGTGGCATCTACTTACGTACGTGGCATAAC ACATGCTGTAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTCTGTC
WI-18908	70 G C ---			TGGAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG/GCJTtagggaaaacattccatcccttgagtcAAAAAATCTCAATCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---			CACGGTTCTCTGCATGTTACCAGAGCGCCTTCTGGTCTAGCCACGCCCTGTATGACCGCGCAATA TCCCCAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTCTC CCCTCCCTTACGAACACA/A/GJAAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---			CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACG/CJCCCTGTATGACCGCGCAA ATATCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA/A/CJAAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---			TTAGGAGGTGGGTGAACCTGCTCCTTGGCAGGGATTGTGACACTGCATTGCTGGGTGTGTCTCT/ CJCGGCTCTTCTGGACCTTGACCGTGGATACCGCATGTGCCATGTGGTATTGGGTCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	---	AGGCCTGTGGCTTATGTACCCAAACAGAGGGTCTCTGAGAAGTCTGGCTGGGATGCCCCCTGGC CCCTCCTGGAAGGCTGCAGAGATGACTGGGCTGGGGAAGCAGAGTCTGGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCCTCTGTGGCCACAGGCACCTACGGCTTCTCTCC AGATGTCTTTGCTGAGCAGACAGAGTCAAGTGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCTCAAC/CATCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161 C T ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21 T C ---	---	---	GGTTTGGGGCATTATTTCT/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCC ACCTCATCTAGAACAACTCTCTCGCCAGACTG
WI-19591b	156 C A ---	---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAAGCCATG AGTATAAGATTAAAGGCAGTTACTTTTGAACAAAGAGTGGCATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTCC/CJATACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAAGC CATGAGTAAAGATTAAAGGCAGTTACTTTTGAACAAAGGAGTGGCATAAGCAACTCAGTGTG GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	---	TCCTCAGCTCTGTCACTCTTGTCTGAGGGTTCTGTGTTACAGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAAGCCAGCTCTCTAGAGCTCCA/GATCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---	---	---	CTCTCCCTAAGGAGCCTTGGCTTGCAGCCCCATTGAGGAGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCTCTCTCT CCCCAGTGTCTCACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGTAAC GGAAGGAAGGGCGGCTATT/GA/AGGTATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	---	GACGTGGACAAAGGAGGTTTAAATGAATACCTTTGTTTGT/CJCATGTTCAAAAAAAGAGATTAAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGGCCATGTTTCCAACCTAGGTTAATAATAA GGCTATTGTCCACCACTCTCGGGCATTGTGCAATATCTCGGGCTCAAGTGGGAGGCCACGTG GGAACAGGCCTCAGAAACAAAGGACATGCAGCCTCCCTGAGCCAGTTCT

WI-19766b	93 A G ---	---	---	TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGGCAGGGCAGG AGATGAACCATAGGAGCCAAAAGTC/GJGACAAACAGAAAGGACACACCAAGCCTGAAACCCCTC CGGACAAAGCAGAGTTACAGCTGAGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCACCCCTCCTCCTACCACCAAGCTCTCCGCCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	---	TGGCCTCAATGACTGGTACATTGGAGAAAGCT/GJGAGCAGCATCCTTTTCTGTGGTGGGCAGGGC AGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAAGGACACACCAAGCCTGAAACCCCTC CGGACAAAGCAGAGTTACAGCTGAGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCACCCCTCCTCCTACCACCAAGCTCTCCGCCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	---	CTTCTCTGTTTGGCTTGCATTTGTGCGATTGGAAAACCATTTGGAAGAAGGGACTTTCTCTGCAA AACCTTAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGGAATTTAGGGCGGGCGTGGGTGGGCTCAGGCCT TATTAATCCAGGCACGTGGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	---	CTTCTCTGTTTGGCTTGCATTTGTGCGATTGGAAAACCATTTGGAAGAAGGGACTT/GJTCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGGAATTTAGGGCGGGCGTGGGTGGGCTCAGGCCT TATTAATCCAGGCACGTGGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	---	GGGCTTAAATCCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGCACACCTTGATACAGATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTCATGTTGGCTCACACGTAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	---	TGTTTGAATAAAAAATTTCCATGGTCTTAATTGAAGTGTATGTTACTTTCTTTAGAATATCCTTTT TTCATTAAAAATAAT/CJCTAAACCACTCTATGTGTTCAACCTTCTGTTAACACTAAGATATGGGT TTTTGGAAGGCCACAAAGTCACCAAGTCCATGAAGTGGCGAATGGTCTGTTTGGAAAGCTCTC CAGGGTGTCTTCCAGAAA
WI-19909a	29 T C ---	---	---	CCAGAAATAAAGCCTGAATATCTCTTTC/CJTTAAAAATAAATTTTCTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTATCTAGGCAATTATAACACTACCTAGGCGGG TTTTTCTTTATACCTTGTCTGACTGTGGAATCACTAA
WI-20341	221 G C ---	---	---	TTGAGAGGCTGAGAGAGGCTGTTGAGACATTGTAATAAGTCTTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTTAGCAGGA GGCAGGAAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATATTGGGTGACGTATGC ATCCCCCATGCATTGGTTTTTTC/JATGCTCCAGTGAGCTGTTGGGCAAGTCT

WI-20113	60 T C ---	---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT/CJGGA AACAGTAAAAGCAAATACACACAATTAGGAGGAATATTTCAGACATAGGATATTTAAACAT CACTCAAATACTGGAGCATGATTCAGCAATAAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ---	---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCGGTGTGGC CACTCCACCAGGAGCAACACTTGACTTCATTAAAGGCAAG/CJCTTTACTCTGTTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	---	CCTGCAATCACAAAAGTGGAACCTAGTTGATATTGAAATCATACTTGATTTAACCACTTCAGAAA TTCTA/T/CJAAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---	---	---	CTGGATTTTAATATTTCTGGCCTAATAACCAAAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGCAGATTCCTTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/GJJAAGTCCACCTCATGAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	---	GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCACTGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGCGGTGAC/TGTCTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAAGTCTGCTGCTGTGTAGAAGCTCTCC
WI-19348b	98 A ---	---	---	GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCACTGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC/GJJAAGTCCACCTCATGAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAAGTCTGCTGCTGTGTAGAAGCTCTCC
WI-19635	98 A T ---	---	---	ATTAGTTGTTGGGCCACATTCAAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAAAATACAGTATTATJATCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTCGACTGCATGCAGATATGTGTCTGAAAGAACCTTTGCCCTT T
WI-19641a	46 A G ---	---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJAGTATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTTCATTTGATTTGTATTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 C A ---	---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATATCCCCCT/CJAGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGTATGGACACAAGTTTTCATGCTATTAA
WI-19673b	180 C T ---	---	---	TCTGCCATGATCACATTTGTATGAAGAACATGATGGTCACTAGTAGGTAACTTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGGATCACCACCTGTAATCTAATAGT GAAAAGGCAATGATGCTCTCAGTATCAGTGTGTAACAACTTTTTC/TCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGCTCAAAAAACACAGCCC

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WI-19673a	35 G A ---			TCTGCCATGATCACATTGTGATGAAGAACAATGATG[G]ATCACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTAGTAGGATTTACCTACCCCTGCTTTTGCATCACCACCTGTAATACTAAT AGTAAAGGGCAATGATGTCAGTATCACTGTGAAAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCACACGTCACAAAAACACAGCCC
WI-19724	35 A G ---			TTTATTGGGAAACAAGGATTGTAATTTGGGTAA[G]CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196 T C ---			TCCTCTCCCCCACTAGATGGTATTGATCACTCTGCCCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTCTTGGATTGCCCTCATGAGAAATGGTGGCTGGGATGGAGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAAAGAACACAGGCAATGTATCCATAGAGCCCTTTAAAGAGACCCG[T/C]TGG AAATGGGCATGGTCTAATTTGGTGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85 A T ---			CTTCCCTCATCCCTCTCCACACACCATCCCGAACAGTCTCCAGGATCCCTGCCACTGGC CATTTGGAGTGTCTC[J/T]TGGGTAGCAATGTGGAACACACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTTGAGGGCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGGTAGGCA
WI-19946	122 C T ---			CAATGGAATGATGAGTGGTGGTGGGGTGGGCGACACACACCTTCAATACACGTCAAGGTG CTTCCAGTTTAGAAAACAGAAATCTGCATCTCAGCTGAGCGACAGAGAGGT[C/T]TCTTCCCTG ACCCAGCGCACTCAGAGCCAGTCTGTTTCAAACTGCAATTTAACTCGCCAGAGAGTTTAC CGTAGGCATCTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 G A ---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAATATACATCAAGTAACCTTACAGCACACATTTTGGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTGGAGAACGACCCACGTTAGCAGCAGATACCTTACAGCTTGTCATCTACTCAA GTGATGGCCAAACAGAAGCTTCTGAACCTCCTCCTGGGAGGTAGCTGACAAG
WI-19076	40 G A ---			TTGGTTGGATACCTTGCTGGAAAAAAGCAGTTTAA[T/G]ATTCAAAATACCTTTTAAAAA GTAATCTAGCACAGATTTTCTGTAAACTAGATTATGTGTAAACTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTTCCAAATCTATCTGGCTCCTGAAAAACTGCAGA AAGGCATGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATCTT
WI-20218	26 T C ---			CCACACACTCTGGTTTATAAGCTA[T/C]JAGGACAGACAGATGGAACCTGAAAAACAGGGTAG AAAAATAACATAAAATGGAGGGGAACAGTGGGATGCAAGAAATGACAACAGCCACATGTGCCCA GTCAATACTTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTATACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 T G ---			CAACCTTTTGACAGGGGACGTGAATTTCTGATGAAAGTTATCTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTATGGGGGGGCTGGGCTACCCCTTTCTCTTCCA TCCAGTCTATTGCCAGAT[G/C]CCAGAGAAAGCGGGGAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTCACTCTCTGTCGACTCCTCATGCTGGACTGTCTTTCGGGG

WI-20361a	192 GA ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAATGGCTTATGCAAGATGACAGAATATGTGAATCTGATGTGCCAGAGTTACACTCTGCACCTCCAAAGCTACAACAGTCCACAGCTGAGAGTTCCCTATACCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTCAAATGGGAAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75 A G ---	---	GAGCCAAACCCAAACAAAATAAACACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCTTCAGAAAT[G/J]TCATAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTTCAAAATTCATCTCTCAAAATTTAAATTTGTTTAAATCCCAAGGTGCTTATGAATCTTCAAAAATAAACTGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 GA ---	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAAATTATAAGTTGAATAAATAGTATACAGCAATCTTCACTTTTAAAGAAAATGTGAGATCCTTTGTTGGTTTTTATTCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCATTGAGG
WI-20593	79 A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTGCTGACTTTCAG[G/J]TTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAAAGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCTTCACCAGACTATCCAGAAGCCATTCCATGGGTTTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCAT[C/J]ATGTATCTTGTCCTGCTGCTTTTAGTTAGCAAGGTGTATGAATCTTTAAGTTTGTCTTTTCTTCTCCTCGTGGTATCAGTGAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATGGCCATGGAACCTGAGCAAAAGCCGTTGGGATAAAATCACTCACTCACCATCGAGGCCACCAGTATT
WI-19066i	239 A G ---	---	TGACAAGGGGAGAGAGGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCCTCGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTT[G/G]TTCTTTTAA
WI-19066g	184 CT ---	---	TGACAAGGGGAGAGAGGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCCTCGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066f	148 T C ---	---	TGACAAGGGGAGAGAGGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCACAAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGGG[C/J]GGTCACCCCTGTAGCTGAATTAATCTTCCATATTCCTCGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA

WI-19066e	147 GC ---	---	TGACAAGGGAGAGAAGGGAATTTACTCATTGCAAGGAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCG[C/T]TGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066c	100 GA ---	---	TGACAAGGGAGAGAAGGGAATTTACTCATTGCAAGGAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGAT[C/G]ATCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066b	87 CT ---	---	TGACAAGGGAGAGAAGGGAATTTACTCATTGCAAGGAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAAC[C/T]CTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066a	72 CT ---	---	TGACAAGGGAGAGAAGGGAATTTACTCATTGCAAGGAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-20660	105 GC ---	---	TTTACAGCGAGTTTTCOCGTCTCAATAAGTATGAATCTAAATAGTATAGGTGAAAGAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGATATTTGT[G/C]TATAAAGGGAAGCATTAATATTTA CAGACATATTTACAAGTTCTGAACATGAGTGATTCATTAATCTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCAAAATACTGTTTAAACAACATATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGTCTCCTGGCAGCCTCCCTCAGTCTTCC TCCACCCGCTCTTCCCTTCCAGCCTGCCTGCATGCATGTGCACCCCTGG[C/T]TTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120 CT ---	---	TTCCCCAGGTTCTGTATTGCAGCTAAGCTCAAATGT[G/T]ATTAACTTCTAGTTGCTCTTGTCTTG GTCTTCTTCCAATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACCGGCAACCTGTAACCTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49 AT ---	---	GAAAGCCAGAGATTAGCCCCGCATTCGGCATCTGTCAACCAGGACAGAA[AT]GCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACITTTGGAGATCAGAAAAATTCATATTAAGCAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18987	35 GA ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCTC[G/A]GTGGCCAAGCCCAGACACTACCCACCTTT CCCCAGTGGCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAGAAAGACACCCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTTCACAGCCCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA

WI-19236	54	G A ---	---	TACACAGAGGTGCGAC TTGGACTCTGAGGGTTGGGTGGAAGGGGAAAGG[G]GATGGAGAC CTGCTCCCAGCTCTTCTGTGAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGAGGT CACCTTACCTTTTTCATAGGGGAAGAGTGTACACTCTGGCTATCTCAGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACTCTGCGGAGGATGTCTGTTGATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTGCTGACCTCCAGCCTTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGAGCTATCTATCTATTCATTTTCATAGCCAA ACAGGAGACCCCTTTCAGGACTTGCACACAGGGAGGCTGAGCCAGGAAACCTCTTCTCCCTGGT CTGGCTCTGCTGGAGCGG[G]CTGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAG[C]AATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGACAGATGTGGCGTCTCTGTGGAAGCCACCGTCTCTCTTTGG GGGCCGCGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TGGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGACAGATGTGGCGTCTCTGTGGAAGCCACCGTCTCTCTTTGG GGGCCGCGAGATCTAGCATCTCTGAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTG/T[C]GGCTCATGGCAGAGCAIT CAGTGCCACGGTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTGCTGCTCAGCTCTCTGCTGTGATGTGGAAGCTTCTGATAATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCCAAGTATTGCTCTGTATTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTTGTTTCAATGGTGGAA/GIGCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCAGTTTAGTTGGGATGATTTGATTTCTGTGTTGTTGATCCCATTTCTAA CTTGGAAATGTGAGCCTCTATGTTTCTGTTAGGTGAGTGTGTTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCTCTCCCTAAAGGGACTCTGCGGAAC[C]TJTTTCACACCTCTTTCTCAGGGAC GGGCCAGGTGTGTGTGTACACTGACGTGTCCAGAAAGCAGCACTT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACTAAGACAAGAACATTTCTCTCATAGAACATTG ATCTGTTTTACAGGAAACAAACCTTGCCCTTGAAATTTACACAGTGAAGTGTACATAATTTGCATGAA A/G/TAGCTATTTTTTCTAAGACATTTTTTCATTCATGAATATTTCAAGTTTTTTCATACTGTACA CATTTCTTAAACACATGATACCAAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263	CT ---	---	CTCTGTTCTGTAAGCTGACAGGGTGACAGCCCTTTCACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGTGTAGGCTGAGTACTGAATGGTCTTCATCCCGAGGAGGGGTGAGCCCGGAGGCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGGAGCCAGCTGCACACTCTCTTTTCAGAGCAC TTATCCACTTGCTCTCTCTCTACCTCGGACCCCTGGTGGAAAGGG
WI-19134a	162	TC ---	---	CTCTGTTCTGTAAGCTGACAGGGTGACAGCCCTTTCACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGTGTAGGCTGAGTACTGAATGGTCTTCATCCCGAGGAGGGGTGAGCCCGGAGGCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGGAGCCAGCTGCACACTCTCTTTTCAGAG CACTTCATCCACTTGCTCTCTCTCTACCTCGGACCCCTGGTGGAA
WI-19224	112	CT ---	---	GGTTTACCAGTCTTCCAGGGAACCTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATACTCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTAGGACAAAGTTGTCATAATCCAGCAGGCCAGAGACTTCC AGGGAACCTCATTCAGGAGGTGAAATGATGGATGACTCCTCCAAAGATGAAAA
WI-19201	179	TC ---	---	GCAGCTCTTAAGGACCACCTGGCCATTAGCTCTTGTCTTTGATGGCATCTCTTCCACCTTGTCTCTC CTTGTCTCTCTGTGTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCTCAGACTGCC CTTCCGCCCCACACTTTGCCCTGCAGGTGACCCGAAAGGACIT/CJTGGGGGATAAAAATTCAAAAA GTGTGATGTCTGCTCAGAGGTGACACTCCATGTCTGCTTGGCTCAA
WI-19034	45	TC ---	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAAT/CJACTTCTATTACATTAAAG GCAACAGCAGTAGTAAAGGTTTTACAGTGTCTGTCTGTTGAAAGTCAATATAAATTTTGTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTCTGTGCGAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25	CG ---	---	TGTTCTGAGTCACGCTGAGGAGAG/CJGCTTCACTCAGGAGTTCACTGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCTTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATCTTAAATCGTTCT TGATTAGTATCGTGAGTTGAAAGTCTAGAACTCTGTAGTTTGAAGTCAAGGGAGAGGATAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	AG ---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCTCAGTGGGGAA/A/ GJAAAAGCATCTNCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	GA ---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCTCAGTGGGGG/G/A/ AAAAAAGCATCTNCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	TC ---	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTTCTTGAGGACACACCTTCACTACAGTTAAACAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCT/CJAGATCCACAATTGCAAGGCGCACTGCTGGCTCA CTTCCTCACA
WI-18501	121	CT ---	---	CAGAGGGAAAGTTTATTGAGTACGCCACAGAGGAACAGAGAAACAGACAAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTGGCAGGACAGAGGGGCG/CJTGACAGCA GCGCATGCCACAACATTCA

WI-18017	87 C A ---			ACAAAGAAATGGAAATAGGTTTGCAGAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCTTAAATATATATCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTAGAAACCCNTCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGATTTTGTGTGACCACCACCTACCACAGTCAATTTGTAGAGCAGTTAAATCACAT/C]GCCAAAATTCCTCTGCTTCTGCTTGTAGTCACTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117 C A ---			CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAAACAAGACGGCCTTCTGGCNCCTCTGCGTCC AAGGCTGTAAGGCTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGGTTCTTCAG
WI-18295	40 C T ---			ACCACACATTTGTTGAGAGCCCTATTGTGGAGAAACAACAG[C/T]TTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATCCCTTTNCCCTTAGCTTCATCTTCATAATGCCAAA
WI-18459b	64 T C ---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGTGGGAGACACAAAT/ CIGAGTAATTAAACAACAATAATTTANATGACAGTCAATTAATTAACTCTGGTAAAGCCAGAG GGGAGGAGGGCGCTTTC
WI-22585	56 A G ---			TTTATTTAAATTTGCATCTCGAGATAATAAATTTATCTGACAAGTGAACAATG[A/G]CAGAAAGC AGCAGTGAAAGTTTCGGAGAGGAGGATATCCTTCATTTTGGCAGAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGATGGAAAATGGGC[A/G]TCTGTGTAGAAATGATTTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTTGCTCTTTGCTGCTCAGAGGCCCTCAGATGGATACGAGCAACTTCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGCAAGTTCTGTGTGACACAGACAG GGAACAGGC
WI-19888a	98 C T ---			GGCAGGATTCACCCATAACAGAGAAATACTCCTTATTGGAACAAGGTTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTG[A/C]TTGGACAACGTTGTAAAGATATTAATGCCACT GAACTGTTCATTTAAATGGTAATTTTCATGTTATGTGATTTTCACTCAATTAAGAATGGAACATGT CTTATAATTTGTAATTTACATGAGANCAATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCTCTCTCAACAAAGAATCAGTCAGTTGAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATTGCTTTCCACTGCCCCAACCAAGAAATTTAATGAATGNCNTTACAATGAGATGACTT GAAAGTTAAAGAAAGGTACCTTCTTGGAGGTTGCATGACAGGATTAGTCTTCTGTGTT[C/T]CTGGT GCAAGTTTGAACCAAGTATTGTTACCATTGCAATCAGAGCATCTGTTTCCCTGTGATGCCACTAG

WI- 20561b	94 T C ---	---	CGTTGCTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC/CJGGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---	---	CGTTGCTATTTAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATT TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---	---	GCITTCATTTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T/AJATAAATCTATATCATATATTTATACACAAAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---	---	GCITTCATTTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGT/AJTAGAA CATATATAAATCTATATCATATATTTATACACAAAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---	---	GCITTCATTTTCTGTCAACCCAC/CJGCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACAAAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTGGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---	---	AAAGATTTCAGTCTGGGACACAGTTTGAAAAACACTATTTATAAGTTGCACATATTACAAACAG NTCCAAATGGTGAACCTGGTATTTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGC/ G/AJTGGAACATAATGTTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC/A/GJAGTCTTTTATGGGGTATTTCA GTTGTTAAACAAAGTTAAATACTTATTGGAACATAATCTTTGTTATTTATTCGAGGAAGAAGATCT ATAAGATTGACTTACTCATTTGACTGGTTTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTTGTGAGCATTTTGTAGAGAAAGTGGTATTAGAGGATACAG CATAAATTTAATTTGTAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTTACTGGTCATGG GAGATTGGATAGAT/CJGCCTAACCTATCTCAATTTTAAGTAATGIGAGCAA
WI- 22091c	205 G A ---	---	GGCGTATTGTGATGCAATGTCCACCCAGTCAAGCTATCATTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGACTCATAATTC ATTACTTGCTGCTAGCTTTTAAAGGTTTAAAAATGTGTAGCATTAAAGTGGTATTACTTGAGGGCA ACA/G/AJATTACGGCTTAAACACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ---	---	CAACTGCTCTGAGGCTTTCACTAGCTGATTTATAATCCTATATTAT/AAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACITCTCAAGGGTGGATATGTGGTGAATGCAGACTCCATCAATATGTGGTT TTGTTGCTTTTGTAGCTTAAGTCTGTTTGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTTCATAAAATCGAACAGTTGAAGGCTGTTTTTTGTTAATTGCTG
WI-21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACTTTTTTTATTGAATTATTGAC TCTGCCCGCTGTGCTGCTTCACTCCAGTCTGTAATGCCCTGTGTAGGTGGGTCCCCAG GTCTGGGCTTCTGAGGTCCTTCTGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGTGTCAGATGGGCAGTTGGCTCAGCTCAGTCCCTGACTCCGGAACACTGTGCCTCT CAAATGATCTAGAGCTCATCTTGGGGTACATGAGGGCAGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTTCAAGCCAAATTCACACTGGGAAACACACCCTCACAGATGCCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAAACATTTTAA/AC/AAATTATCTA
WI-21449b	222 C T ---	---	AACAGCAGAGTCACTCCAAATGCAAAAAAATTACAATTTTTTAGAATAAAATTATAATGTTTA TAATGCGGTCAGAAGANTTGAAGGTACACAGAAATCAATCACGCAGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGTCCAAGCTGACAAGAGTCCCAACCTGAGAGGCTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CTTACAGAGCCAGTCTCTCTGGGTTAG
WI-21558a	157 G A ---	---	GCCTACAAGGAAGCCTGTGGACAGCGAGNITGGTGAACCGACTCCAGCCTGGAAACCTGCCCTC CCATCCCTTTAGCGCTTCTGGCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGTGGGGGGCAGTATG/AJAGCCAGGGACTCCCTCCACAGATGAGGCCTAGGGCTGCAA AAGGGCCCTGAAAGAGAGATGTGGTCAAGGCTTTATGGGCTCTCCACC
WI-22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCTGGGGCCTGACCAATGGGTGATTACATTTAAAAACCAACCAACCAACCAACCAACCAACCA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCCTGACCAATGGGTGATTACATTTAAAAACCAACCAACCAACCAACCAACCAACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---	---	TCATGAATATGCAGCTCCATAATCTTCTCCCTTGTAAACAACTGCAGTCCGTTCAAGCTGTAAA AACAAGCCCAACCCCAAGACATCACAGAGGCAAGAGCAGTGGCAGTGAAGAGGAGGCTGTAAAG GATGTTTCAAAG/G/AJAGGGTCCGGCTATGTGCCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---			TCATGAATATGCAGCCTCCATATCTCTCCCTTGTAAACAA[C/T]GTGCAGTCGGTTCACAAAGCTGT AAAAACAAGCCCAACCCAAAGACATCACAGAGGCAAGAGCAGTGCGAGTGAGAAAGGAGCCCTGT AAGGATGTTTCAAAGGAGGTCCCGCTATGTGGCCACTGGATGAGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGCGAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---			ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGGTAAAGCCCTGACATCATGGTCTTTGTGATCTG[T/G]ACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGCGAGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---			ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAGGGCTCA CAACTAAAGATTTACATGAAGGGTCTGATTGATTGAGCAATCTAGGGATATGTGACAGGG TTT[C/A/G]TGCACCTGGTACAGAACAACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---			ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAGGGCTCA CAACTAAAGATTTACATGAAGGGTCTGATTGATTGAGCAATCTAGGGATATGTGACAG GGGTTTCATGCACTGGTACAGAACAACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATACTTATGTGTACTTCTTG[A/G]TTTCA TCATACAAGACAAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG[T/A]AATACTTATGTGTACTTCTTGATTTC TCATACAAGACAAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---			AGCCAACCTCAAGGCCAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCATTTGTAAATAA AAGAATACTAAGATTAGATGAACACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGAGGAAC AGATGTTAACAAAAACAAATTAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---			CTCTGAACCTAAAGGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCA[T/A]ACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAANTGCACAAATCTAACACCATGTTGAAATCATGCTGA GTTCTGGAGAAAGTTAAAGTGTAATAATTACAAAGACTGACATGCAACTCTTACCTTACATTATT CATCTACAGACTATTTCTCCCTTAGGAGATGAGGAGTATGGGCCCTTAGGT
WI- 22130b	165 C T ---			TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGGGCTGCCTCCCTCTCTCTGACAC CAGCAAGGGGAGGACCATCACCAGCCCTGCCCATCATGCATCCATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGGT[C/T]GTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

WI-21661	117 G C ---				GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAATAAACATTATACACATATAAGATCAGT CTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAATAA[G/C]TTAGTCACAGTC ACACAAAACCTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTTAAATTTGTGCTTTAGCTATGAAG GA
WI- 21980a	25 T C ---				TCAGTTTAAACACATTCATCAAGGA[T/C]AGATTAAATTAATGTCCAGGTGAGCATAAAAGGGAGATT TAAACAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAAATTCAT GGTGAAGCCCTGGGATAAG
WI-21636	71 A G ---				TGCTTGTAATTAATGTGGTGTACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTT AAA[G/G]TAGCAATATCTATTATAATAATATTGAAATAACACCATAATAATATCATAAGGA AGTAATCTAATTGTGTTGATTTTGCAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI- 22457a	112 G A ---				TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA CAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACAG[G/A]CAGTTAATTAACATAAG GAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAATACCTGGGGCC AAAACCCACTGAACCTCACCCAGCTGAAACACATGAAGGATACTGGGTAAGGA
WI- 21524b	97 C T ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATGATGACGCTGATGACGACCTTCGCGTCATACT AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTGCAAAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTCTCCAAAGTTACTTCTCCAGGGGATG
WI- 21524a	35 A C ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATGATGACGCTGATGACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTGCAAAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTCTCCAAAGTTACTTCTCCAGGGGATG
WI- 22652a	32 G T ---				TTACCTTCCAAACCCAGGCCACTTTGGAGAAAG[G/T]AAGAGAAATGCTATTAAATCAATAAGCCAAGAC AATAGGGAACCTGGGGTAGACCAGATGGGCAGTCACCATACCATCATTCCTGCCACAGAACCC TTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT CITTAGGG
WI- 21703d	197 A G ---				CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGGCTC TGCATCCCTTTCTCAGCAGACAGCACCATTTCACCTCTCTGGGAAAGCAGCATGGAGCCTACACCA CTTGCTTTTCTCACCAGGGTAAGAAATGCAGGTTATTCAGAGGGGAGTGAGTCTGGGAA[G/G]G TGGGCAGAGCAGCATAGGGGCAAGGACTTAAGGGAACITGTGGGGGAAGAG

WI- 21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCGAGGGCTC TGCATCCCTTTCTCAGCACAGACCATCTTACCCCTCTCGGAAAGCAGCATTTGGAGCCTACACQ A/GCTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG TGGCAGAGCACAGTAGGGGCAAGGACITTAAGGGAACCTTGTGGGGGAAGAG
WI- 22663c	139 G A ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTACAG GC/GA/GAAGAGCTTCCATTTGCTGAGGGCTTTTCCCTGAATCCGTTGAATGTGGGT
WI- 22663b	55 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCTGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTAC AGCGGAAGAGCTTCCATTTGCTGAGGGCTTTTCCCTGAATCCGTTGAATGTGGGT
WI- 22663a	38 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACCTTAC AGCGGAAGAGCTTCCATTTGCTGAGGGCTTTTCCCTGAATCCGTTGAATGTGGGT
WI- 22668	99 A G ---	---	TCCTTTATCTGCTGCTGCTGCTGAGTATCTGGGAATCTCAGGATTTGAGGAGCCCTTGGGATT CCAACTTAACAAATTAGTTTCTGTAAATATTA/GTTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAACCAATTAATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACTTTTATT
WI- 22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCCTGGCTCAGTCTGA/TCTAGCACCATTTT CAAGTTTATGGCAAGGATTTAACCTCTCAGGCTCATTTTCTCTTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI- 20258	157 G T ---	---	AATCCACACTTTCACGGAGGGGGAACAGCCTGCCATGCTCCAGGCTCACAGCGCGGGCTAC TCTGCTGGTGGTTGGTGAGGTGGAGATGGTGACGGCGCATTTGAAACCGTAAGGCATGACAACG GGAGCCCGCGGGGTTCAG/GTCCGTTGACGAGGTGCATGGCTGGCAGCGGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTCCGGGGAAGTACC
WI- 22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAATAAATACATTTTACATTTGTAGAGAAATCTAGGGTCT ACTAAATAATCTAGTACTGTTTCCACTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/C/ATGAGTAGGGGGCAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAAGGCTGCGGAGGGCTG/ATCTTAGAAGACATTACCCA AATGATGAGAGGCGCCAGTCTGCGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAT AGCAAGTGCAAAGGGCTGAGGGAGAAATGAACITGGGCTTGTCTACAGGTTGAAAGCGCGCCGGT NTGGCTGAGGTTTAGTGATG

WI-22724	117	A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGAAGTGTITAGAGATATAGGA CAAATCAAGATTGTCAAATGTATAGTAAGCTGTTAAAGCTTCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAAT
WI-22750	48	G A ---				TGTAACCTGTGTTTTCCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCATCTGACTACCTAAAGGAGAGTCAAGCATCTGACCATCTGACTGTGCT
WI-22775a	60	A G ---				TGCTGTTCTTTAGTTTCATGACGTTTATCACAAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTTGAATCCTTTCATTGAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAATGAGGTATGAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	C T ---				CTTTAGCTAATGAACTGGCTATGTGGACTATGATAGCAAGAAAGCTACCCAAGTCTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCTCTGCTGCTTGAGCCCTCATCCCAACCCCTCCAAGCCCTCATGCCACACACCGTGTCCACATT CCCCATCTCCCTGTCTGCTCCCATCTCAAGTCCAATTCOAAGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTG CT[G/AT]TGGCGTGGTATGTTGGGGCCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGGG[C/T]CTCTGTTCCCATTTGTCTCCACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTCAGCAGCCGAGAAAACACACACA
WI-21314	122	A T ---				CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCTTATCACTAT GACTTTCATTTGATTTTTTATTGTTTCTTCCATTTCTCTGTCAAACCTTTTC[A/T]TTTTTTTATAA ACTGTTTTCTAACTTCACTTAATTTCTCTATCTGTATTNCTTGATGTTCCCTGAACCTCTTTTAGAGG
WI-21186	95	G A ---				AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCCCTAAGTGTGCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCTCTTCTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGATTGAAT
WI-21187a	94	A G ---				CCACGATAACTATAAAAGCAGAAAAATTAGCTTTGAAAAATCAATAACATATTTAGTAACACACATT CATTTTATAAACACACATAAAGACACC[A/G]GNNCTCAGTAATGCTCTAGTCCAGGGTCTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39	T C	---	TTTCCCACATACCAATGCACCTGTTTGTATAAACTATT/CJGTGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATTAACAAATAATATTAAATCTGTACTATTACTGC TTTAGTTATCTAGTTATTGAGAAAGGAGAAGTCAGCATAGTTATTTTCCATGTAATAAAGCTT AACACA
WI-19937d	186	G A	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACTATTGCACAAACCAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185	C T	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACTATTGCACAAACCAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227	C T	---	GAAAACGGGGTGTAAACAAAGAAAGTCTCAGATCCCACTGAAAATCTGTTACAGTTTACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTTACAGGCTTCAAAATACATTTCTGGGG TCCAATCACATACTTTCAGGTTTCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTATTTTCTTCTACTGAATCTTGGGTGGGAG
WI-21122a	42	C T	---	TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACCTCTGTTTTC TTATTCAAATGTACAAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACCTGGAAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53	A G	---	CAGTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGAACTATCCACAGGAG[G/G]CAAGGAGAAAG CTGTTCTCTGG
WI-21054	23	G T	---	AAGGAACTGCATGGGTACAAAT[G/T]TCCAATTCATACCTTAACAAGGTGGGGAACCGGGTCATTCT TGGCCTGCTCCAGAACAAAGGGGAGTCTATGCACCTCTG
WI-21059b	181	T C	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCT/CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT
WI-21059a	63	C T	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT

WI-20442	37	T C ---				TCCACGTGAAGGAGAAAAAANGGGGGGGGGCTT/C]TAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43	T C ---				GTGACAAGAGGTGAAGCAAGGGGACAGGGGCGAGGCGAGT/C]CTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C ---				ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGGAATGCTACATCTGGAATTT/C]CATTAC ATCAACGTTAAATTTGTCCGACCAGTCTTCATTGCTGATCACCTTTTGATAATGACAGATCCAAACAT GAAACTCCTGAAGCAAAATGAATATTACCTTGTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACAGATCTAAGGAATTTGTACAGGGATCTTCT
WI-21149a	167	G A ---				AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTATTTTAAACAATGACCTTATTTATCTTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACACG/A]TGTCTCAGAATCGGGCAGTATTGCACAATGGTT TGGGCGAGTTCTGTGGTTAAACATGGGATGGGATGGAAACCCAGGCTCTACCTG
WI-21376b	188	A G ---				GGTGTCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGGAAAAACACTTTCAATGTGTC TTCCATTGATGAATTTGTTTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAACCA GACAGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGATGAGTTCTC/A]G]GAAGTGATTCT GAACTGAGCAGCACTCATGTCTGCATGGGGAACCTCTGGGAGAAAGAGCCT
WI-21382d	125	C G ---				CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAAAATCATGAACAGAACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAGTGGGGGGGGTTTGGATCCAGTGGGATNGGCTTCCQ/C]G]AGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCAGTCTCTGATGGGGAGCAGAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGTCGAGGAGAGCTGCTGCTCCTAGTCTCGCAC
WI-21437a	201	G A ---				TCCTGAGGTTGGAGTCTAGCATAGTCCCTCCCTCAAAGAGGGAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCCTTTGGATGGAAAGTTTCTGGAGTCCCTCCATT CTATTCTGTGGGCGAGGAACATGCCAGGGCTGCTGTTAATGGCAGGGGTCACTTTACCAGGGC/G /A]CAGGCATAGTGTGGCCCTGNCCTGCCCCCTGGGGGCCACCCCTGGGAACAGT
WI-21202b	156	A C ---				CAAAATAGAAATTTCTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGTTATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGAGGG AGGAGGAGAGATTGACCA/A]C]GTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C ---				CAAAATAGAAATTTCTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGTTGA TCTGTTTTATGAACATGTTATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGA GGGAGGAGGAGAGTTGACCAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATATTAACCATATTTTACATAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAATCCAAAGTCATCTAATAATTAACCATATTTTACATAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---	---	GGATTGAGTCCCAACTTGATCTCAATTCACCTTCTTGTCATGTAAACAAGCTCAATCCCTCTAAAGTT TCAGTT[C/T]TTCACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCATTGCTCTGAGGTTGTTGTCCTAGGACTAGGTAGGATCTCTCTTGCCTTCTGCC TTACCTAGGCATAGTGCCCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68 G A ---	---	CGATGCTGCTAAGATAGGAGTTAATCTTTACATGGTGAGTGGTCACAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCAGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCCTCTATGAGAC AGCAGTCTGGCTTCTTAAACAGTAAACCAATCAAAAGAAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGGAAGGCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATTCAAATGTACATGTAAATCCAAATTTAACAGATCAAAATGTTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTCACTTTTAAGAAACATTTATAAAGGTAATT AAAACTCTAGGTGTATACCTT[A/C]ATGGAACCTAGTTTATTCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTTATAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAATAAGAGGCCAATTTGGGTC ATTTGAGAAACATTTTCAGCAATACAGTGGGGGACGGCCGTTCCGCTCCAGCTGGGTTTCCC AGATGCAACAAT[C/T]GGGGTTCTGGCTTCTCCACTGGTGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAACCCCTCCACTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACCGGGCAGGGAGGGGACAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	TAGCCCTCTGCCAATCTGGCAATNTGAGGCTGGGGTGAGCTTGGCCGTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGACCTGGGCAGTGGCTCTTTGGAGAAGGCA[G/A]GAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCCTATTTCCCTCCCTGAAG

WI-21475b	117 A T ---			TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGGCTCCAAACCCAGGCTTCTC/ATJCTTGTCTACTAAGCA CAGAGTCTGAAGCTTGGACCTGGCAGTGGCTTTGGAGAAGGCCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTCCCGTTCTCCACCC/ATTTCTCCCTGAAG
WI-20893d	207 A G ---			TGTTTGTTCCAGCCACATCTTCTCCAAAGAACCCACCCAGCCGCTGTGCAGGCTTGTCTGCAGGG CTGTCTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTACGTAAGTTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAACCTGCCATTTTCTCTCTTTTACAATGCAATG TTC/A/G/ACATAACATTTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI-20893c	179 T C ---			TGTTTGTTCCAGCCACATCTTCTCCAAAGAACCCACCCAGCCGCTGTGCAGGCTTGTCTGCAGGG CTGTCTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTACGTAAGTTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAACCTGCCATTTTCTCTCTTTTACAATGCA AGTTTCAACATAACATTTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI-19941c	71 C G ---			GAGCTCAAGGGAGACCCCTTACCCAGATAGGACTAACTGGAGGGTGAAGGAAACAAGGTGA GGTATC/GJGGTCTGGTGAGACAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTTATCCAGTGATGTCCTCTTAAT AACTGGGTACAGGAGCATTTNTGGAAGGAGAACCAAGGACAGAGACAAGCGG
WI-21552b	166 C A ---			TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATCGATCTCCTTCACTCAAGCATTTATOCATAGTGTACAAAGAA TCCAAGTATACTCTTGATATTTAAAAATGTA/C/A/AAATTAATTTATTGAATTTAGTTACCCC ATTGTCTATCAATATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21552a	66 G A ---			TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG /A/TAATAATTACTTCAGAGTAAATCGATCTCCTTCACTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATACTCTTGATATTTAAAAATGTACAATTAATTTATTGAATTTAGTTACCCCA TTGTGCTATCAATATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21512	54 C G ---			TCCTCGTACTTCATGCTCCCTCCCTCCCGCAGAACCTTACAAAATATTTCTGT/C/GJTAGAGAGGA AAGAGCTGTGCTGCTCTGGAGGCAACGTCAGGTCGGGAAAGGCACTCGTGGTCTGTGATCTGTC TCAGTGATGGAGGTCTCCACTCGCCACAGGAGCCTCGGGGCCAGAGATGAGAATATGCTGTAA TCCAGTACAGGGGCTGCTGCTGGGGTCCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---			CACATAGTTTCTCAAGAAGAGGATGAACCTGAAAACCTCTCTAAGGCAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAAATCTTTAATTTTATTTCTCTTTAATACTGTCAAAATACACCAAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAAGTGTAA/G/AJAGTAG TATTCTACATACCACAGTATACAATGATGCCTTCTCTGAGGTTTAGGAAC

WI- 21514b	133 C T ---	---	TTGAACCTCGAAGGTGGCTTATGTCTCGACTCCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGAAAGGAGCAGCATACCATGGAGC[C /TACAGGACTCCAAAGGACTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTAAAGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---	---	TTGAACCTCGAAGGTGGCTTATGTCTCGACTCCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGAAAGGAGCAGCATACCATGGAG GCCACAGGACTCCAAAGGACTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTAAAGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	ATGAACATGTTGCAGTGGGATGAATC[G]TTATCATGTAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---	---	TTATCGGTTCTTAATACAGTACAATCCCTTTGTTGAACAAAAGTCACACTGGCAATGATTATTTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAAACATTG[A/G]TCTAGTTCAGTGATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCACCTTGGAAAGTGACTACACATGGCAATA AGCAGCTATCTCTTTACCAACCAAGATTTCTTGGGCATGTGATGGCCAGACCCCTTTCCAA GGGAATA[C/G]TACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGAACAAGGCCACAGGC AGTGGAGGAATGTGATGACTTCACGTGTTTCAGANTTCTAAGGCCACAGCAT
WI- 21574a	235 C T ---	---	AAACCCAGAAATTTAGGTACTTTTGATTATGAGGAACCTCACTACTAGGAAGCAACTTATGAGTG TGTAATAATTTGATCTAGCAGCAACTTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTACTGCCTACTTCTCTCTGTCAGGTGGGA
WI- 21644c	151 T A ---	---	TGACTGCCAAGATTTAGGCCCCAATTAGGAGCAAGGGTCACCTTAACCTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT[A/G]TTCAATCAAGATCCATGGAATGATGCAGTTTAACATGTGTTCTCAGC TTGCCACTGACCACCTTCTCTTTCTAAATATGGCAACAGCAGCAAGTC
WI- 21614b	55 G A ---	---	TGCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]JTTTAAACA AACCTCATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTTATTTCTAAGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---	---	GACCGAGAAAACTGCAAGGCATATGATGTTTGTGGAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATATTAAGATAAGGATGGACT CTTTCAGTGAATATTATCTAGGACACAAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCATATTTGGCCAAAGGGAAGGTAGGATGGGTACTGTGTGGAACGGA

WI-21981	61	T A	---	---	---	TGTCATCTCATTTCTGGAGAAATCATAGATGTGGCAGAAATACATATTTCTTGAAGAAAAAAATTTA/GT CTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACTGCATGGATAGGATAGA CACTCTGTTCTACAGATCCGTGCTTTGGGAAATTACAGGAACATAAAAGGATATAATGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAGGTTAAATTTGG
WI-21660	120	C T	---	---	---	TCCCACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACAGCCTCTCCACTGCT TACTGTGTGTACCAAGAGGCAGAAAGCAGCTACCCAAAGCCTAACCTGGC/C/TJTGCTTTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGAACTGGGACTGGGAGAACCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211	C T	---	---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAATAATTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGGTCATAGACACGGGTGAGCTCATGTGGAACTCCTCCTT GTCTGAGGTTTCCAGGCTGGCACAGAGGTGAGGCGAGAATNTGGGGTCCAGTGGATCTCCOC ACAACTTC/C/TTCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33	T C	---	---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAATAATT/CJGTGTCCATGTGGTTTGAGTCTGTTAAGAA GGACATAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGTGGAACTCCTC CTTGCTGTAGGTTTCCAGGCTGGCACAGAGGTGAGGCGAGAATNTGGGGTCCAGTGGATCTC CCCAACTTCTCTCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81	C A	---	---	---	CAAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGTCTTCTAGCTTTTACAATAAGNGGAGG GACCTCTGACTGCA/C/AJCCCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35	A G	---	---	---	CAAACCTAGTCACTCTACTGATGCAAAATGATTTGGJ/GJGGTGTCTTCTAGCTTTACAATAAGNGG AGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198	T C	---	---	---	TCTGCCATATTGTTCCAGCACCACTATTACTGTATTATTTCTCTTGAGGAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCTAACTATGTGTTAAATCCTTTTCTTACCCAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTACT/CJ AGAGACAATTCATAGTTTCATAATCTTTTCAGGGTTGTGCTTTACTTTGCGGGGCG
WI-20934a	72	T G	---	---	---	CCAACATGCAACATAGTCTTCATTTCTTAAAGATACATAGTAAAGGTATGAAAACATTTGTATTCA GAGAA/T/GJTTAAAGACAAATGGTCAAATATTCAAATGGCTGGCCTAGTGGTAAATCCAGCAGAC AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAATACGTGCCCCATTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCCAGGAGA
WI-21581	55	T G	---	---	---	TTTCCATTTTATCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCT/GJCCCTTTAAC CTCTCCAGGCAAGGAAAAGTGATCATATTTGAATTCCTCAGAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAAGTAAAGAGGCTTGAATATAATGATATAAATGGTAGCCCTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTTTGGATGTCATTGTCCCCA

WI-21961c	200 T G ---	---	---	AGCTTGCCTGAAAAATTTGGTACTTACTACCTTTGCAATTCCTTTATTTATTATTACTTTTATTTTCCGTAAGTTATTGGGTACAGGAGGTAATTTGGTTATAAAGTCTTTAGTGGCGAATTTGTGTAATTTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGGCCCCCTTGGCTCCCACTTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGTC
WI-21961b	73 G A ---	---	---	AGCTTGCCTGAAAAATTTGGTACTTACTACCTTTGCAATTCCTTTATTTATTATTACTTTTATTTTCC[G/A]TAAGTTATTGGGTACAGGAGGTAATTTGGTTATAAAGTCTTTAGTGGCGAATTTGTGTGATTTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGGCCCCCTCTCCACTTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGTC
WI-21956	26 T G ---	---	---	CCCACTGGGCTCTTTCAAGTGAATTTGTTCCCTTCGTTCTTAAAGCCCTTTTAAAAATGAACCTCCATTCCCTGCTGAACTTGCCTTACTGCTTTTCTGCTCATGCCCTCAGTCGAAATCTTTCTTCTGAGGCGGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGGTTGACGCCGCTAACTCAGGGTAACTCTATCTCTCCACCGGTACAGAGGGGTTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	---	CAACATACATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATATTTTGTAGAACATGAGTGAGAGTGTTGTGTGTGTGTGGCGCGCGGCACGGCATGGCACTGAGGGGATTGCAATGGG[G/A]AACAGGATAAAAGGTATAAAACCTTGGTCCGAAATCTTTGCTTATTAAACCTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	---	TATACTGGTTTTGGTTACATGGATGAATGCTAATGGTGAAGTCTGAGATTTTAGTGTACCCCATCACTGAGTAGTGATGATGATACCCCACTTGTAGGCTTTTATCCCTTACCCTACCTTCCACCCCTCCCATTTTGAGTCTT[G/C]CATAGTCCATTATATCACTCTGTATGCCCTTGCATACCCATAGCTTAACTCCC
WI-21139a	165 T C ---	---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTCTGCCACTTAACTAAGTACCTTGAGCAAGCCACTTAATTTCTGCTCTCTCTGTGAAATGGGTACAACTGTGGGTACGAGTAAAGGAACATAACATTC[G]TACAGCACTTCAGCACAAAGCCCTGGGCACACAGCACTGCATGGAAATACACAGGTAAACATTTTAAACAGTGGGGACAAAATTTTAAGTACGTGGCCAGCTGTGGTGTCTTGTGGTCATTAAGACAAATGTTAAGANTCAGGAGTACTTAAAGTGTAGTGGTTACAATTTTGTCTCTTCTCAGTTTTTCAATTAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAAGTATTAATTAATTAATTCATATTTTGAAGGCTACTCT
WI-20317b	217 G T ---	---	---	CAGGACTTGGTTTGTCTGCCCACTGCACATAAATGTCCCTTTTGTGTGAGTTATGGTTGTGTGGGTTTTTCCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTGTCTTTATCCGGATGACGGAGGGTACACGGGGCGTCCGCTCAGTTCGCCCGGACGAGTATT[G/A]CTGAACCTGGGACGAGTCTACTCTCCCCCACAGGAGGCCACGATTTCAAATCCTCTTTTGTGTGAACCTCT
WI-22082e	179 G A ---	---	---	

WI-22082b	67	CT	---			CAGGACTGGTTGCTGCTCCCAACTGCACATAAATGTCCTTTTGTGAGTTATGGTTGTGTG[C /JGTTTTCTTTTGCATAAGAAATATGTCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGTACACGGGGCTCGCTAGTCCCGCGAAGGACGTATTCGCTGAACTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139	AG	---			AACACAACTCCATGCTTTCAAGATTTCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTGGTACAAATACACATATAGCAATGATACAAATTAGGGGAAACCCCTGG GCTTCTJGJTAACAAGTGAGTATACATTAAAGACAGTATTGCAGAATGGCTTCAGGATTAATTTGA TTAATTTAGAGAGAGCCTATTTCAGGTCTTCCTAGCTCATCCACACATCACC
WI-21723b	125	AG	---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGTCAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	GA	---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGTCAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	TG	---			CAACAGATGCTTGAGCCAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTTJ/JGCCCATTTCTCTAATCTCTTTGCCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCCTCTAGTTTAAATGCTCTGCCCAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	AG	---			TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCCTTAAAGAACACATACACACATGTGCACACAC[G/A]GAGGCAAGTACAAAAATGTAACC CCACCAAAGTGATGTAATGAAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	CG	---			CTGAGGCCTGCTCTAATTCATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAAGATTGAT TTTCTCTTTGTGTACAAAGGATTCAAATAATTTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG CTJGJCAATACACACCAAGCCAAAGCGTAACCTTGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	GA	---			AATGAAATGCCACCCAGAGGTTAACAGCTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG[G/A]AATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACATCTGCCAGGGTAATAGGCATGGGCAAT

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WI-21079a	50 G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGT[G/A]GCGAAAATCAAGT TGTTTAAATACCAGTGTGCAGCTTGATTCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCTGAAATATCTGCTAGTGGGAATTTACAACCCACTACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAAATAGGATGGGCAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTAACTTTTAAAGGAAAAGT[G/TT]TATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCATAGTTAGCTTAACAGTTAACATTGAAGCTTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTTCAAAATAATAATTTGGTTGCAAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAAAGGACTCGGAAGATGTTGATCCAGGGCAGAGT GAGGGGCAGAC[A/G]GGATGAGGCTCTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCACACCCACCTCACC CAGCACACAGGCACACGCGAGGGCACACGACACACGNTGCACTCACACACGC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGCAGCTCAG[C/T]GGCTTCCCACCTCTTGGTACCC GGTTAACTGOCAGNGGTTGACAGTGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGCAG[C/T]CAGCGCGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGTTGACAGTGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTAGCTAGCTAGTCCAGGNTTCTGGCCCCCAATTTCTGGGTTCTCCCCAAG CCCATGCTTCTTCCACTTCTCACAATCTTTACTTCTCCTCTGACCCCTCACCACCCCAAAATTA/G JCTTTTAACTCTGGAAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACCCCTGGCCCTGCCCTC/TJAGCTGCATGCCACCCCTC ATATCCACCCCATCCCCAGCTCCTGCCCGACACCCCAAGGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCACATAAATTTCTGTTGATTTTGCCATTACCCATAAAATGGTGGGATCTAGCTCCCT CCTTGCAAATTTGAGCTGNNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTCTTACCCCTGCGCTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCAATTTATTTCCCTCTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTCTTGGCCACAGTCGTAACATTGC

WI-19891c	172 C G ---	---	TGTTGGTCTGAGAATTACAGCTTACTACAAGGAAGCTGAGAAATTGCTTGGTGGCCCCCTCCOCCOOG ACTCCTCTGTCTGGGAAACGTGGCTTGNCTCCAGACACGTGTAGATGCCAGCTCTCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/GCGTCTTCCGGGGGTGGGGCGTGTCTGT CAGGACGGCGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---	---	GCACCTGTAGGGGTAGCTTCCATGGTTCTCAAGCACGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGC/TGCAAACTGCTTTGAGGAATNTCCAGGAGGAATAAACTAGAAGACGC ACCTGTATTTTACCATACTATGGAGAATACAGTAATGAAGTGGTGGCAGAACTTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTTGTCTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAAGTGTACAAT ACATTATGTCAGGATAAGGAGCA/TGACACAGGATTTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCGACAGAGGCTGGGAGGCGGGGGTGGTGGAA
WI-20270a	53 G A ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCG/TATCAGTGTAC AATACATTATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCGACAGAGGCTGGGAGGCGGGGGTGGTGGAA
WI-20622	130 T C ---	---	CCACTTTCAATATTTACAAAATGCTCACGCAAGCAAAATATGAAAAGCTTTCAACACTTTCCCTTTGTA ACTTGTGCAATAAATGCAACTTTAACAAACATACAAATTTCTTGTATCTTAAAGTTGAA/T/C/ TACTAATTTTATGATGTTACTCATATTTTATTCATATACTTTAAATGACATCATTTGCCAATACATA CAATATTTCTNTAAGTATTTTACAATAAGCCAAACATCTGTATGCAG
WI-20768b	190 C T ---	---	TTCCACTCAAACTCCACCCCACTTCTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAACTCATTTCTGTATATCACCACCTTA CAGGAGAGGTCTATTTCTGGGGACCCAGAGN/CAGCACACATCTGCTGGGA/C/T/CAGGGGACTC GTAATTCGCCTTGGTCCAACTCTTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	TTCCACTCAAACTCCACCCCACTTCTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCA/C/T/GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAACTCATTTCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGGACCCAGAGN/CAGCACACATCTGCTGGGACCCAGGGACTC GTAATTCGCCTTGGTCCAACTCTTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAAATATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGACCTAAATAGGAATATTTGTTGTCATCTTTAAAGAAA TGCTTTAATACATACCAAAGI/TJAGTGGAAATCAATAGATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACCTAAATTTATTTCTATGTATGGAAG

WI-22202	128 A G ---	---	---	TGTTGCTTGGTTGCTTCTGGAAACATATTGGAACACTTGTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCATTATGAAATCTGAATTTCT[A/G]TTAAT ACTCTGGTGCAATTCATCTGCAAAAGCACTGGCACAACCACTCTTGCCTGGTGCAAGCTCTCGG AGAACATCTAATATTGAGTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AA[C/T]GAGGCGAGGAATGGGCATGGCGCTGCGGTACCAGCCTGGACGTTGTGCTTCCAAAGTACAC TATGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGCATCATAGAAAAACCCCTCAGCCAGAGTTAGGACATTGTGATCTCAGCCACTAACGA GCTGATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGGTTGT[C/T]TCATTTGCAAAATAAAACCCA GACCGGTGTCATCTTTAGTCCCTTCCAGCTCTATTTATGATTTGCTCTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGGGTGAGAACCTTGGCTTTT [C/T]TTCCAATCTCTCTTTAGCCAGAACTTTGCGAGAGCCCCCTTNNATTTCTCTCCCTCTATTCC CCTCCTTTCCCAATGTGCTAAGGTCCCAATTCACAGACCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCATTGCTCAGTACCAGA[A/G]TTTGAGTAC GGTCTGTTAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGTTGCCATCTCCTGGTGGCACATCTATACCACTCTGGCTCTGAAAG GCTTGTAACCAAAATGGCAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTTGGTCTAGCATCCAGCTCTCTCAGCAAGGAGGATTGGT[C/T]CCTTGTGTTTTCTG AACAGGGCCCGAGGCGAGCCAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAAT[A/G]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCCTTCAACCAGCTACACTTTACCTTGATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTTCTGGACAGTTTGTCTTATGTTTCAGACAATCAAGGNTCCCTTCCAGGCGACGCCAGTGCTT [C/T]GGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTCTGTGTTTCGTTTTCCTTTTGTGAGTAAATNAGCAATACACTGA[T/C]TGGA ATCTGCATGAATTAATAACATTAAACAAGTTCATAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTGACACATTCTCCTCCTAGTT T

WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTAAACAGTCTTGAGTTCCCTCTTTAGGCTTCAAGA TAAATTGTGATTTTCATCGCACCCAGATACCTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTGAGCAGACATTGCCTGTGCTCTCTACCCACGACGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTAAACAGTCTTGAGTTCCCTCTTTAGGCTTCAAGA TAAATTGTGATTTTCATCGCACCCAGATACCTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/CIGCTCTCCACAGCTGATTACAGACATTGCCTGTGCTCTCTACCCACGACGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTAGTCCCGAGTCGAGGTGCATTCTTCTTATCTTGCTTAAGCCACTTGGGTAAAC TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGAGTCCCTGGAGGGAGGCTTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT/CJGAAAAAATACACAATGGGAAGTACACA
WI-21965a	112 A G ---	---	CAGGTTCCACACAGAGGCTTTATTTAGCCACTCAGGACCCCTGGCTTCTGCTCCAAAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCGACAGCCAGJGCCCCACAGGTTCTCTGTT TCCCAAGTCTGATGGATTGAGGCAAGACCTTACACATTACCCACTACCTGCTGGAGAGGAGGCTC ATGAGGACGCTGTGGTCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAG/CJGTTCTTATGATCAGAC CACCTCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGACGAGGAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTACAACAAAGCGAGGTTTAAAGGAGCCTGAGAAGAAATTTCAACAATTTGACTATACAGAG TCTTCAATTCACAAAACAGTTAATAGTAACCTTGGTGGCACATACACATGCATTGAATACCTCTGTAT TATTCAGTAACATAAT/CJAGGNTCCTGCATCTCTCTTCAACA
WI-22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTGATAGTGGGTTATATGGGCTCTCTGCCTCCTGGCTGTGTTATG/CJ GGANCCAGGAGTGGAGGAGCCTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGTCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTGATAGTGGGTTATATGGGCTCTCTGCCTCCTGGCTGTGTTATG/CJ GGANCCAGGAGTGGAGGAGCCTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCTCTCTCAACACCTCCAGGCCAACCCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGGA GCCACAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACTG/CJGJAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTCTGGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149 C T ---	---	GCAGCATTCTCTCCAAACCTCCAGGCCACCTGGGGCCAGAGCACTCATGCCACGACAC CTACGTGGCCCGAGTACGACCCGCTGGCCCGAGGTCTGGCTCTCAGGACGTCCCAGCAAGTGA GCCAGAGGTTTGCTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTGGAGTGCTTC TTTGACGGGCGCGGTGCTCAGCTGCTCTCTGGAGGTGAGGAAGGAGGT
stFIBBb	412 G C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCAAGGCCCTTGCACCTGCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCAAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGAGGCCAGGAGCCTCTCTGA AGGACCATGCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGGAGCATGAGCCCTTTCCCAAGGCCCTTGCACCTGCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCAAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCAAGATGAGGCCAGGAGCCTCTCTGA AGGACCATGCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stIGLV2	61 T C ---	---	GTCAAGAGGACGCGCTCTGGGACGCTCCACCATGGCTGGCTCTGCTGCTCTCACIT/C]CTC CTCACTCAGGACACAGGTGAGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTC TCTGCTCTCAGGCTCACCGGGGCCAGCACTGACTCACTGGCATGT
stSG1001 7c	70 T C ---	---	GTTGAGGCTCATCTTGAACCTCTGGTGTCAAGCATCTCCACCTCCGACCTCCAGGGTCTGGGAT TAIT/CIAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33 G A ---	---	GTTGAGGCTCATCTTGAACCTCTGGTGTCAAGCIG/A]ATCTCCACCTCCGACCTCCAGGGTCTGG GATTATAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63 A T ---	---	TAATGATAATTAGGGCACTTCTCCACACGAGATGACACAATTGACCCAATATCATTTGAGGC[AT] AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA
stSG1009 6	36 G C ---	---	GTGAGAAAGATCGTCTTCTCCCTCCCATGACQ[G/C]GGCTTCCGGGGCACCTGTGCGTTTCC ACCCGAGACGGCCTTTGTAGGGACCCACTGCCACTCCGCTGCTGTGGCTGGGTCCGCTCTCTAG GGCTCGAGTGTTAAG
stSG1011 8	107 C A ---	---	TAGGCTTAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGCTGAGGGCAGTACCTCCATTGGGC ACAGTCCAGACCCAAAGTCAAGATGCCCATCTCTGGC[C/A]CTCAGCCCTCAGTCTCTCTCTCC ACGAGCCGCTGCTGTTTGTAGTTTTCTCCCAAGTGA
stSG1012 0	89 T C ---	---	TAGTAGGTAAGAAAGCAAGGAGGATTGCTTATCGCATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTACGAAACACTTAATAIT/C]GTTGTGTGTAATCTGATTTATCTCGTCTTACAAATG
stSG1017 8	42 C T ---	---	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAAGTCCG[C/T]GGGAGGAGAAAGTGAACAGGAA TCGATTCTTTGCTTTAACTGCCCTTAGTAGGAGAIGTTAAATACTTGGC

stSG1019 3	136 GA ---			GGAACAATACCTACCTAAGGACAAAATACTATTATAAAAAAAGTCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC T[G/A]TTTGAAAACGTGAGATTTAAGTTGCAAAC
stSG1020 2c	143 GT ---			AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGCTTTCCGAGGGAAGCTCAGTCTGGCTTGGGAG AGTCAGCCTTGGTCACCTCATACGGGGCTCCAAAGCTAAGCGTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCA[G/T]CAAGACCACAAAGGCAGATGCCCACTGCTGCTCTCTTCTCTTGTCTACTTCT
stSG1020 9b	75 AG ---			TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAAATCTCCTTAAGATCCCACCTTTAT TTTTA/GTCTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1020 9a	34 CT ---			TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/TAATAAACTAAATCTCCTTAAGATCCCACCT TTAATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1021 8	29 TC ---			TACTAGACATGCAAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTTCTGA
stSG1025 2	108 AC ---			ATAGTTTCAGGAACAAAATCATTAATGGAATAATGAGAAGAAATCTTTATTTTGGACCAATTTT AGGCACCTAAGAGTTTCTTTCTCTTCTCTTCCCTTGATCA[A/C]AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915 0	123 AC ---			CTGTATTAATTAAGAAGGCACCTAATTAATGAGGGACGGAAAAATCTACCTGTACACAAAATCTGTAC TTTAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG[A/C]ATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166 TA ---			TTTTTTGTTAAACCAACCCCTGAAAAGTTCCACATGTGAATATAGATACAAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAAGTATCTATACACCCAGTAAACAGCAGGGC AATTAGTCAATTAATAAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTAATTTACAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGAGGAGTAATCCTGG
EST14096 8	71 GC ---			GGGATGTATATTACAGATAACACAACCTCACAATAATACCATCAGACATTTGAAAACTAAGGCCATTCT GTGA[G/C]TTATTTTAAAGCTGGTGTGTCACATAATGATCTTAAAAAAAATGAATTACCAAA ACCAAGATTCTCTTCTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---			TGCAATTTGTGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTGTCTAGATGTGAGGTGCG CAGGGATGCTTAAGTCTTCCTCTGCGCAGAGACCCGAGGTGCAGAGATGATTTCTTCTCA[C/A]CCCTTC TCTCAGGGTCTGGAG
EST22555 7	60 GA ---			TCAAGCATGTGTAAAGGCACTGCCCCGCCAGACCTTCTAACTCTGCACACTGGGAAGGT[G/A]AAA CCTGGGAGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

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EST22917 6	74 C T ---			GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACGAGGGGCTCTTGGGCTCTCAATGCA ATAGAAAC/TTTGACATGGGGCCAAAAGACTCCAGACAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---			CAAGTTAGAACCATGTCATCAGCTTTTCATCCATGGTGTAACTTAACCCCTCAGGCTGTCTACTCA/A GTTGGGTTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56 A G ---			GAGGGGAACTTCAAAGAGGATTCCAACAGTGAAGCAGAATCATGGGGCAAAAGTC/A/GTCTATGG GGCAGACTGAGGTTGGACACACAAAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGGAGTAGCCAT
STS- R37410c	201 A T ---			TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCATTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGTATG T/A/TTATTTGAGTGGTGCTCTAGTGGCCAAAT
STS- R37410b	139 G T ---			TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCATTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATG/T/GTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAAT
STS- R37410a	48 C T ---			TGTGACCATACCAACCTATGCAATAAAGAAAGAAAAAATCCTCA/C/T/JTTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAAT
STS- R42778	74 C T ---			TATCGTGGGAAGTTCCAAACCTCATACTTATGCTGCTTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCTC/C/T/JTTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA
UTR- 04350	125 C G ---			CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAAAATGTTCCGGACCTAGATA/C/G/JTGACGA AGGTAGCACGACACTGTGAGTGCACTAA
sISG1026 6	55 T C ---			GAAATAAATAAACTGCAAGCAATCACTGTTAATAAGAAATGTTCTTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
sISG1028 2	70 T G ---			GTATAATTCAGCATAAAGCCAAAGCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT/G/AAGCACAGTAGTACAATAATTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
sISG1031 0	128 C/A ---			CACTTAGATATGAGGAAAATGTTTTAATGGACACAAAGGAGTCAGCCACGTTGGAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAATAACAGCAAAATATTTTTCACCT/C/A/JTG TCAATGCCAATGCATTGAAAGGCCAGAAAATGAGAAAAGGATAACAAACCTTTTGTATAAAAAGGTA AGAATTTCTGTGTG

stSG1033 1b	116 T C ---			TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGATGCATTTCCGG GCTCCAACTGTCTAGGAAGCCTAGACCTCAACACCAACCTCCAT/CJGCAATTCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---			TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGATGCATTTCCGG GCTCCAACTGTCTAGGAAGCCTAGACCTCAACACCAAT/CJGCAATTCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTCTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---			ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGAGTTCGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTG/AJAAAGTATTTAGACCAAAAGGAGGT
stSG1345 b	60 G A ---			AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACATAGTTTGCCTTCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1345 a	54 T G ---			AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACATAGTTTGCCTTCTTACGGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1385 b	117 T G ---			TTAATGTCATCCAGGAGGGGCCAGGATGGAGGGGAGGGTTGAGGAGCGAGAGCGAGTATTTT TGGTGGGATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTGTTGTTCAATCAATTAAGAA GACAAAGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTGTCG
stSG139	69 T C ---			TCGTCCTCTTCCAGTCTTCTGCCAGAGCATCCCATGATGTTGTGACCCGACAGCACCTTTGTGTCT TT/CJGCTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCCACTGATTGTGACTGTCTGCTGCCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGTCAAGGCTGTGTTGTCAATCCCT TGGCTCCTCCACTCCAGTTTGGCTTCTGCTCTCAT/CJAGTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGCTCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---			CCCTGGAGTTTCTGAACATAGGAAGAAATGCAAGTCATGTGTAGGTCC[A/G]CTCCCTTGCATGA AATGTGGGAGAGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---			CAAAACCAAAATCCTCCACGATATATTACTATTAGTCTAAGT/CJTAAATCAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAATGCTTTCCTTAGTCTGCAGATGGTGA
stSG1483	44 T C ---			CACACCCACAAGTTTCATGTATGCCAAGTATCAACTCTTGAGGACAAGGCAAAACCAAGTGCA [C/G]AATGTGGAGGATGTCTGTTGCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGGAA AATGCTGA
stSG1696	67 C G ---			

stSG1847 b	95 G A ---			TTGAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAAATGCTACCCCTAAAAATGAAAGAATTT AGAGGTTAAATAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTGTTTCCAATGTGAAACCAAAATTAATAAATGATGACTGTGCT TCAAACACAACCTG
stSG1847 a	49 C A ---			TTGAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAAATGAAAGA ATTTAGAGGTTAAATAAACAAGTGAGAGACCGTTTACTTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTGTTTCCAATGTGAAACCAAAATTAATAAATGATGACTGTGCTG TTCAAACACAACCTG
stSG1897 a	83 A G ---			CTTAATGCCCTTCTCTCTCTGACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[G/G]GCCACCACTTCTCTCCCGGCTCCCAAGATGACT
stSG2022 a	86 T C ---			TGCTTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAACACAGGCCCTTTGTGT TGTTATTTTCTCCCTACAAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---			AAACGTTGTCCCAAAATTTGTTTCAGTTTCACAAGTATAAAATAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTTGACATT[C/G]ACATCAGAGTGGGCAATTTT
stSG2108 c	71 A G ---			TTGAGCAACAATGATTCGCGAATTTGGGAGCTCCAAACCAAAATGATT[C/G]AGGGGCTCCACAGAG GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---			TTGAGCAACAATGATTCGCGAATTTGGGAGCTCCAAACCAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATATCTCAGAAATGGCAGCACCCTGGCATGGCGATGGTGCGAGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAG[A/G]AAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCAGTGGCATCTGTTGCTCTG
stSG2141 a	113 C T ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATATCTCAGAAATGGCAGCACCCTGG[C/T]ATGGCGATGGTGCGAGGTG GGTGCAAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCAGTGGCATCTGTTGCTCTG

stSG2148	50 A G ---	---	---	TGGGAAACAACCGGCTATAGTCTGAGTCATATATTTTACACCGTGATTTTC/GJAAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	---	CTCAATGAGGACTCCATCAGCCCAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT [C/T]GCCGCGTGACTCAGCTAAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGGAGTGAAGGACCA
stSG2189	41 C T ---	---	---	CAAGTGGTGAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACATCATCGCTAACTTTGAGCACCTTAGTGTCTGAGTACTTCGTATAGGTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTCTGTATGATG[T/C]TTTATATTTATGTAT AATGTCCTTACCTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	---	CATTTCTGCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGTCTAAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/ C]CTGTCCAGAACTCTCGCCAAGCACTGGGCTGTCTCCTCAGGAGAGAAATTTCTCCT
stSG2306	67 A G ---	---	---	GTCATCAGCGTAGAGGTCACTGGTATAACAACAGTAGCTATATGATATTTGGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACTGATGAGGTGAACACTTTCACCTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	---	GAAAACTACCCACAGCATCATGTTAAAGAGAGAGATGAAGAAAAAATCCCGCGAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGAGGGTGAATG
stSG2339	63 T C ---	---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAACGTGTCAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGTGCTATTTCTGGCTGTGCTTCTCTATTCATCA
stSG2465	76 C T ---	---	---	CAAGACTAAGAGCCGCCGCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACACTTTTGAGAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	---	TTGCAGGCTTGATTCCACAATAACAAAGTCATGTATAGAGAATGTGAATGATACTTGAAACCAA GATATATAAAATATTGAAGTCATTATGCCCTTTTATGACTGGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	---	AATTGCCAAATGGAAATTTCCAGAGGATTTTATAGACCAACTTTGCCCTGTTCGATTTCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCCGAACGTGTGAAAGCA[T/G]GAACAATC CCGGCCCAGATTAAATTAT
b				

stSG2577 a	121 C T ---	---	AATTGCCAAATGGAAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTCACGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATC CCGGCCAGATTAAATTAT
stSG2700	58 G A ---	---	ATCTCTGAGCTGCTTAGTGGGAAAGGAATCAATTATTTATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGGGGAATAAACCAGTGTCCAGAGCAGAGGAAGGCTACTTGAGCCGGACACCA
stSG2724 b	101 T G ---	---	AAACAAGCTTTGTCAITTTCCACTACATTTGTTGTCCTTATATTAATATTTGCAATGCTATAAT TTAATACTTATATCCAAITTGCTTGCAATATC[T/G]TTTTTTTAACTCTGGGTGTTGAAAGAAC
stSG2776 a	65 G A ---	---	GTGGCCGATCTTTACTTTCCAGAAAAGGCGGTAAATAAAAACTGTAGAAAGTCTCGAATATGC[G/ A]TATGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAAACCACAAAA ATATCCACTAATCCCGAATATAGTAACCCCTGCTTGTCCGAATG
stSG2791 b	109 G T ---	---	AAGGAAAGGTGGAGGGAAGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTAATAATATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G ---	---	AAGGAAAGGTGGAGGGAAGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTATCTTCTGAACGGTAAACTAGCAATTTTAATAATATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85 C T ---	---	CCGCAATTTCAACACACATCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAACAA[C/T]GAACAAAAATAAAGAAAAGAAACCCATGAAATGCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A ---	---	ATGGGTGCATTTAAAGGCAATTAATACTTTTCAGGCAGGGGCTGGCAAAATTTAATGAGCTGA TGTGTCCCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
stSG3031	71 T C ---	---	ATACTCACGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCTGCGCATTTCTGTGGTGCAGC AAA[T/C]GCCCTTTATTTTAATGATTCAGACATCTGGGCAGCATAGCT
stSG3058	81 G A ---	---	GTCCCAACTCCTCTCCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAG[C/A]TGAAGAAGCATCAAGGCCAAAAAGGCAAACTGGCTGAGGC
stSG3092	94 T G ---	---	CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTTGTCACTATTGAAAAACAAGCCAAAGTTC CAAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATCTCTTATGGTTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G ---	---	AAGAAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTTGTCAGTGGAGTC[A/G]GTGGGGTCTAAGTGTCTGAAGTAG
stSG3245	160 G C ---	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTACACACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGT[G/C]TGTACTTGGCTTAAGTACTTTCATGCTTTAT

stSG3265	42 T C ---				AGGTGAATGAGTTACTAAATGTAGCATTTATTATAAGGAAT/G/CATTTGTGAATAGTTTCTCAG TTTTCATTATGGAAGATGATGATTTCAGCCCCACATTCAGTGTATGTTTCTAAATAACACATCGAC AGGACTGCTGTTGAGTACAAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTGTCAGCTGAATTTCTGGGCTTTATGTGGCAGTGTGGTAAAA
stSG3269 b	141 C T ---				TGTAATGAGTGTGTCATCTATCCATTCCCTTCCCTGAGCCTGGACTGCTTCCAAAGGAGACTAGG AGTGAAGGGAGGAGTCTCCAAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]GTAGATCCCAAGTCCCTGACACATTTTCTTAAGAACT
stSG3269 a	24 A G ---				TGTAATGAGTGTGTCATCTATCCATTCCCTTCCCTGAGCCTGGACTGCTTCCAAAGGAGACT AGGAGTGAAGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTAAGAACT
stSG3284	130 C T ---				TAACTCAAGAACTTTCAGTTACAGGAAGATTTATCTAATATTAATAATGACTAAATACAAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTGTTAATGCTGTAATGGGACATTTGTTGTTGATCTACCC
stSG3292	99 A T ---				GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCAATGGACAAGTGACTTAATATCTAA[AT/TA]ACAAATCAATAGCATTTTCCTAACTTCAA
stSG3323	26 C A ---				TAAATGTCATATCTTTAGTCTCACT[C/A]CCAGTGTATCCATTTTCCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCTGTCTGGACATTTGATATAAATGGAGTGTGCTGATCATGTTGAGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGAGCATGGTCACTTTCATTCCTTTTAA
stSG3369	69 C T ---				GATCCCCAGTATTTTCTAATTTGAACCTTGTGTTGGAAATAAAAAATCTGAGGACCACCTCAGAG GG[C/T]ATAAGGGAACCCCTTTTGTCTTAGTTCATAAGGACTTTCT
stSG3398	125 G T ---				CAAGACTGTAAAGAACGTAGGCCCTTGTGAGAGTGAAGGAAGGATGCTGAACTTGCCCCAGGACTCAGG CTTCAGCTTCAACAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3416 a	43 A G ---				TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGTTCAAGTGATCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3424	173 T A ---				GTAAGACAAGGTTTGTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTGTGATATTACAGGTGTAGCCACTGCCCCCGGAGCTTTTAAACTGAAT GTTGAAATCACTTCTGCTCTTTGCTGGGTAACTGAT[A/C]AAGTTGCTTAACCTTTGTGAAACCAC TTTCTTATCTGTACAAATAATGGACAAACAGAACTTTTCTTCTCTC
stSG3436	88 T A ---				GTTTATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGGAGGCCCTCACAGA ATGAGTGGCAGAGAGGGCCCTT[A/GAAATAGCTTACTCTGTTTCTCTATC

sfSG3463	103 C T ---	---	---	GATACAGAAGATAGTGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAACAAAAATGCATACACAGCTCAATGGGTAC[C]/TJTGGAACAAACTTGGCTTACTATATTA CTGA
sfSG3491 b	71 G A ---	---	---	CAAGATACCTCATTGTCTTAAGTAGTGAGTGGCAATAATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTTAATCTTTACTGGCACCTGTGGATTCTATTAAACTCAATTTACTATTCTTCTGTGATG ACAGAAAAATAAGTTAAC
sfSG3523	33 C T ---	---	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTT[A/C]TJGCATATATGTGTGTACAAACACACACACC CCTAATCTCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
sfSG3536	213 A G ---	---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGTACAAAACCAAAATACAGAATGGCTTC TGTGATCTGGCCTTGCTGAAACGCATCTCACTGTCATTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAG[A/G]TCTGCTGGGTGTTCTCAGTCTTGGCATGAAGTATG
sfSG3583	112 G A ---	---	---	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCCAAAACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
sfSG3586 a	60 G C ---	---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGTGGTGGT[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
sfSG3589	101 T C ---	---	---	ATATAGTGTGTGGTAGCATTATAAATCCTTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCCACCTGGCACAAAAACCCCAATGAT[C/C]CTATTCCAAAGATGTATCCAGATGAAA GTATCCAAACAAAAAGCTATATACAC
sfSG3590 a	70 A T ---	---	---	GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAA AAA[A/T]TTTCTCTGATGCTCTTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
sfSG3619	78 A C ---	---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
sfSG3644	40 T C ---	---	---	ACATATGTAACCTGCCATTAGTACCATATTTAGGATGAGAT[C/G]GATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTTATGAAATAATAAGTTATCTGGGGAACGGCCATTGTCCAAACATTTACTAA GTGCTACTA
sfSG3646 c	70 G A ---	---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]TATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

siSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATA[A/G]TATGTCTT ACTGGTGATATTAACTTTGATACCTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACCTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85 A C ---	---	ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
siSG3693 a	30 C T ---	---	ATTGTTCCCTGAACATTCCCGTGGTCTCC[C/T]CTGAAAGCCGATGACCATCCAACCCCTGGACTCA CCTGAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
siSG3698 b	145 G A ---	---	TCTTGGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACTTCCCTCACTGCAGA
siSG3698 a	51 C G ---	---	TCTTGGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGTTG[C/G]TCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATACCCACCCACTTCCCTCACTGCAGA
siSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGGTCTCTCTGCTGGATCCCCAACTGGAGCCATCCCTGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTCT
siSG3725	104 G A ---	---	GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACAGCCAAACAGCAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
siSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGTTTCATACCTTTTGTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
siSG3787	49 T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT[A/J]AAAGTTCCTTAAGA CACTGAGGGCATAAAACCAACAAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
siSG3880 b	115 G C ---	---	GACAAGAGGGAAGAGATCGCCAGAGACAGGGCTGGGGCAGCTGGGGGTCCCTGAGTGCAGGGCGC CACCACAGTCTGTGGTCAAGGCCCTCTCTGGGGAGCAGGTCTA[G/C]GGCAGGAGGATGCAG GGCTGGGAGGGGACCCCACTCGGGGACCCAAAGGAGTCCATTCTGCCCT

stSG3880 a	36 G C ---	---	GACAAAGGGAAGAGATGCGCCAGAGACAGGGCTG[G/C]GGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACACACAGTCTGTGGGTCAAGGCCCTCTCTGGGAGCAGTCTAGGGACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGGCCCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTG[G/G]TTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCCAGCTCTGGTGGAACTGGCTTCCTGATAACA TCATCTATTTCACTAAATGTGAACCTGCTTTCTTTT[C/T]CAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCTTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTCAACCTTCCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAGTGTGA[G/A]AAATATATTTAAGATTTCCCTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCCTTGTGTATGTATCA CCCCA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGGCT[G/G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACTGCTTACA
stSG4033	123 T C ---	---	AGAAGCCTTGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAAGCTTAATGTTTCAAGCATAAAGGTACTTTT[C/T]GTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCACGTGTACAGCCACGCCTG[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCCGGGAGAGCACCTGAGGGTTCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAACGAAACAAAAT[C/G]GGTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTTCCTAACAGAGATTATTAACTTTTATCAGGTGT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[G/C]GATACTATTGTCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTTTCCCTCAGAGAGCCCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---				CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTCT[AG]TATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128 G A ---				CACGAAACAGATGCAGCCTACACAGTCTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGAGAGGCCGCACTCCCTC[GA]GC AGGGGACCAACGGAGCGACAGGTCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---				CACGAAACAGATGCAGCCTACACAGTCTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG [A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGAGAGGCCGCACTCCCTCGGC AGGGGACCAACGGAGCGACAGGTCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---				CATTACCCAGAACGCCATGGAGGACAGAGC[GA]CCACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCCGGGGCTGCTCTCTCCCGAGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGGATGACCGGTCAIG
stSG4301	81 T G ---				TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTGTGGCTCCCACTTTCCAT TTAAGCAAATAAAT[GA]GCTTCTGAGTAGTGTTCACAGTTTACCCCAACATTTTG
stSG4331 b	71 T G ---				CTCACAAGGCCCAACACAGAAAAAGATACAAATCATTCATCCAGATAATTTAGTTTATGACAC AGAG[GT]TTTCAACAAGTTTAAAGTGTACCTGAAGAGCATGTTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCTCGCCCTTGATGCTGTTTGAAGGGTGTGC
stSG4340	76 G A ---				TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAAGTCAAAAACC ACATGTTCTC[GA]TAAGTGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---				TTCCCAACCATTTGAGTGACAGAGCT[CA]GAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361 a	24 T C ---				TTCCCAACCATTTGAGTGACAGAGCT[CA]GAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376	73 A G ---				TTTCACTGCTACTGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGTCTCTCAAGGGGAG AACAG[AG]CTGGAACCTCGGCTCTGCAAGAAAGCCATCTTCCAAAGCCATTTCTCTCAGCTGC
stSG4381	50 T C ---				GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTTCTTT[CA]GAGCTTTAGT ATCCACAGTAGTGATGTCTGTCATGTACAAGTGTCTGCCAGAACACCCATTAAATTCATGCC
stSG4410	79 A G ---				ACCAATGGTTCTGCTATGTGCATCCGATATTTTTTGCCGATCTGAAATCTGCAAGGGCTTAACCAT TCAAAACACCGC[AG]TTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65	C T ---			AGCAGATCAGTCAGCCCACTTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430				---	TJGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGAGGGAGGGAATAGGCAC
a	54	A G ---		---	AAATGGAATTCATCTGCTGCTCTCTCTCAGGTC
stSG4448	99	G A ---		---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGTIAGIATTAAACATA
					GGTAGGATCCAGTTCTCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
					CCTCCCTCCCTCTCTCCCTCCAGTCTTTCCATCTGTTCCCTCCCGCCACCCAGGCTCT
				---	CGCTAGCCCTGCCCTCTGGGTCACCTG/C/ATGGGTTAGGCCCCCAAAAA
stSG4449	92	T C ---		---	ATTAGCCATTCACTTGCAACAATTGCTTTACTGTAACAGAGTACTGTACTGATGATGTTTACAAT
					TAACTTTGGACAACITTAACCTTAT/CJTAGTGACATTTGCTGTCTAATAATCAATACTTCATCATA
					GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
					CAGACATGAGGGATGGCCCTGTCTCTCTGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
stSG4467	42	C A ---		---	GAATGAACTCAAACTCTTCAGTTTTTAGAGTCAATTTCTGGTATCGAGCGACACACCGAGGAG
				---	CACACCTGCTTCCAAGGCTGCTGCCCTCTGCACACAGT
stSG4475	21	A C ---		---	ACATGTCATTTCTGACCAGG/CJTATTAATAGTTTATTTAGAACAAATGAGTTGAAGTGAGCGA
					TTAAGAGACACAACCTGGACTTTTGTTCTTTACTGTAGCACCCAGGTTTCATG
					GTAACATCTGGGGTGGGGTGAGACAACA/CJAGIATGAACCAATTAATTAATTAATTAATTAAT
					TCAAGGAGACTTTTAATCTAGTTAATGTGAACGACCCATCAATGTTGTGAGGAAAGGGAGA
stSG4477	32	A G ---		---	TGAAGTCTTGCTCTGGGCAACGTTTGGCCTCATTGCGTCACTGAGCTTGGC
					TGAACTCAGAGCTGGTGGGAGCTGCAGCGAGGGGCTGGGGCCAGATGAGCCGCCGGGA
					CAGCAGGCTG/CJTGCCACGCTCTGGCGTTGGTAGAAGAGGACATAGGCTGCCTTGGACTCGATCT
stSG4531	79	C T ---		---	GATTCATTGACAGGGGAGACGCTGTTGTCATCAA
stSG4550					TGCATTAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
b	86	G A ---		---	AAAAGAGACAGTGGGCAC/CJCAATTTGAGGGGAAGGGGCGAGGTTTAGAGAAC
stSG4550					TGCATTAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a	85	C G ---		---	AAAAGAGACAGTGGGCAC/CJGICCAATTTGAGGGGAAGGGGCGAGGTTTAGAGAAC
					AATCAGGCACAAGCTCGGGAGAGAGCCAAAGCTCTTCTGCAC/CJATGGGAGGGAGACAC
stSG4590	47	A G ---		---	CATTGAAAAGGCATGTTCTCTTCTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
					AATCTGTATCACCCAGCGCTGGT/CJCAATGTACTAGTAGCTTTCCACAGGGATTTTTTACTATTTC
					CTATAAGGTTTTATCATGAATAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCACATTTATCT
stSG4623	22	T C ---		---	TAATATCTCTGTTCAAGATGCTCTGGAG
					TAAAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTGTAGTTTTTGTATTTTTCAGATTTAAAG
stSG4843	102	A C ---		---	GTATTTCTTTCTTAGCTTCTAAATTTTGAGTCAT/CJATCAGAAAAGTCTTCCCTACTCCTCAAGGTGA
					GAAAGGA

stSG4850 a	38 C T ---			GGAACTAAACTGGGAATGCCGAGGAGGAAGGGGCTC[CTGTGCACCTTGACGTCAGGCCACGTGAGGAG AGCCAGCGTGCTGTGGGGAGGTTTCCAAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86 A G ---		---	AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGGTCCTGCTTTGCAAGATGGCCTG CCCTGGGACTGGAGCAG[AG]CTTGGGTAGCTAGGTGAGGGTGGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---		---	ACTGGACTGGCTGCTTGGTGAOCGGCTGAGGGGGTGGGACTGCGGCTGACCACTCGCTCTTCAG AGACTGCCCGCGGTGACCACTACGCTCTGCC[GA]GTGGGAAAGCAGAGCAGGACC
stSG4896	112 C T ---		---	AAACAAATCAAAACCCCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTGCGCATAGAGA GGTGGGGGCGAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCT[CT]CAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---		---	ACAGTCCCGATGGTTACACAA[GA]TTGTAATGTATTTAATCCCACTTACGAATGATTAATAATGA TAAATCTTATGTTTATTCATCACTACCAAAAGGCTGGGTGAGGGGTGCTGTTTCTGGTCT
stSG4950	24 A G ---		---	TCATGACTCCGAGGAAAGGTCT[AG]CTTAGCTTCTCTCCCTACTTTCCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---		---	AGTACGGGCAAAACACTGGGATGGCTTCTGACAACTTAAGAGGTCTCCGAGTTATTTCTGGGT GGGAACACTGACCCAGCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTTCATGAGCC CC[GA]GTGACACAGATGGGGCCCTGCTCTATATCAAC
stSG4961	91 C T ---		---	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA[CT]AGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---		---	ACTGGTGCCTCTCAGCAGATTCAGGGGTGCTGAGGGCTGGTTACCAAACTCAGTAGGAGTGCAA GGGCT[AG]TACCCCGGAGCTAGACAGCCTGGGTTGAATCTCAACTTCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22 T C ---		---	CAAAGGAGAGTAGGAGCCCCAA[CT]CTTTAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTAGAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAT
stSG6312	37 C T ---		---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAAC[CT]TATGCCATCGGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---		---	GCTCTGGTCAAGCAAATTCAGGACAGCAAGCAAGGAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC[GA]TAGTTGAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACATTTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGCATG

stSG8145	97	C T	---	---	TTGTGGACTTCAAATCTTCTCAGATTTTAAATGACATTATGCATGTACATATTTTAAAATTT AGACACATTTTAGAAGACACAATTTGTGAATC/JACAAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGTCTGTGAAGG
stSG8150	36	A G	---	---	ATTGTTCTTGAATTCCTGGATTTTTCAGAATAGTJG/JATAAATAATAACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAAT GGGAAAT
stSG8340	30	C T	---	---	AGAGGATTATGGAGAGAGCTGGCAGGATC/JTCAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAAAACGCTCATCAAAA
stSG8466	111	G A	---	---	TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTTGCACACTACCTJG/JTGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--	--	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTCGAGTACAAGGATCTGCCGTCTCCCTGGCTGGGGGGCCAAACCCGGCTTCCATGA GGCCATTGGGACGTGCTGGCGCTCTGGTCTCCACTCCTGAACATCTGCACAAAATCGGCCTGC
ESTD-ADA	--	--	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAAATCCAGGGTCACTGTTCCCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACCTGAGCTGCAGACCC GCAGACAACTCCTGAGCTTCTGGGCCCTCTGAGCTTGTCTCTC
ESTD-AK-168	--	--	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	---	AATCCAGCACCTTTAGGAGGCTGAGGCAGGCATATACCAGAGGTGAGGATTTGAGACCAGTCTGA CCAAATGGTGAACCCCATCTCTACTATAAATAACAAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGGCGAAGGTTGTGGTGAGCCGAGAT GGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAACTCTGTCTTC
ESTD-ANT1	--	--	---	---	TCCTCTGTCATTCCTACTCCATTAGTTCAAGGTGAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGACTGCCCCAACTCGGAACAAGAAGGGCGCAGTGGAGCAGGAGTATTATGCTACGGGGTTACCTT TTTTATGGAGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	--	---	---	CCAGGTGTTGTGGCACGTGCCTGTAAATCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGGCGGAGTTGCAGTGAGCTGACATCGGCCACTGCACCTCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD-APBS	--	--	---	---	GGAGAATAATGGAGCCTGTGGGAAGGAGCGCTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTGACGTGTGGAAACCAATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATAATTGACCCCAAC

[illegible]

ESTD-C7	--	--	--	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGGCAGTGCACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCTTTCCCGGCCTTCCTCTCACACAC
ESTD-CB23	--	--	---	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCCGGCCTTCCTCTCACACATACACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCATACCTCTTCCCTTTCCAGAGACCTGAAAAACGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAAGTGTTCCACCCGAGTGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACCCAGTGGAGCTGAGCTGGTGGGTGAATGG GAAGGAGTGACAGTGGGGTACGACAGACCCGACGCCCTCAAGGAG
ESTD-CB25	--	--	---	---	---	GTTTCTTTCCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCCTTTCTCTCTATCTTTGCGCGTC TCTGCTCTCGAACCCAGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTTGTCACAGAGCTTACCAGCAAGGGTCTGTCTGTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGGTG
ESTD-CB27	--	--	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTAGCAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGCCTGGTTGCATTTACGAGGTGCTGTGGAGTTCGTCTCATCACTGACCTATCTTCTGA TTTAGGAAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TTCCTGTTTCATCTGATGGAAGTCTCTCAACACCAATTTCCATACC
ESTD-COL2A1c	--	--	---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCCCTGTCACTTTCAGGGTTCAGGGTGGAAAAAGGT GAACAGGGTCCCGTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCGCTTTG GTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD-COL2A1d	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGACCTGGAACACTGGACTTCTTCTACTGACGACAGAACACTTACCC AAGAGAGATTAATGGCAAGATATACAATACAATTTTATTGACCAAACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAGTTAACTTCTGGGAGATGAAAAGCTACCATCACTTCTCATCATGAAAAC TGGAGGCCCGGCATAGTGTCTGCTGTAATCCAGCATTTTGAAGGCTGAGGGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAAACAT

ESTD- CTLA-4	--	--	--	---	---	---	ATGGCTTGCCTTGGATTTCAGGGGCACAGGCTCAGCTGAACCTGGCTACCGAGACCTGGCCCTGCAC TCTCTGTTTTTCTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCAGCAGCGGAGCATCGCCAGCTTGTGTGAGTATGATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	---	CAGGCCAGGTGGTGCAGGTGGTCAACATCCGGCAGAGAACAGGTACGCCACCACTATGCACAGGT TCTCATCTTGAAGCTGCTCTCAGGGTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	---	AAAAAACAATTTAACACCTTTTCAATCATATACACCAATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTTCCAATTACTTGAATCTAAATGTCATAACTGATTATGAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTTATGCCCATAT CTGCATGTC
ESTD- D17S93	--	--	--	---	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTTGGCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATOCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAAGCTCTCTGGGGCGGTG GGGTTGTGGCTATGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACTATTGCGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	---	TTTGAGACCACCCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCATCGTAATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCCAAGATCACACCACCTGCCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	---	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAATCCAAATAAGTACACTGTAATAAGAAATTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACTTATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	---	AGGTTCCACATTATTGCTGATGTTTGGTGTGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCTC AGAAGTGAACATACTGCTCCTAGAAGCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGATGAATATAATAATCTGTCTTTATTTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAAATGATTTT CTTAAACAATAAACCTTGAAAGTCCAAAATTAATCTCTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCAATGTTTCATCAGAGCCCTTGGGTGACCAAGGTGTTT GCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	---	CTTTCATGCAGCATAGGCTTCTCTACTAATCACAGAAATTTTGAGAGAGGACAAACAACTTTCAAGG ATAATGGGGCAATCACTTCTTCTTCTTTAGAGCTACCGG

ESTD- D7S399	..	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTACAAACATTTTCATCCAGTCCATCCATAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	--	--	---	---	---	GTGGGACACCCAGGGCTCCAGGCTGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGCTCCTGGGAGAGGAGGGAGTGGGAGGGAGACA GAATGCTGATTATCTGGTGGAGAACAGAACTTCTGGCTGTGGTGGGAGGAGCTGCTTCCAAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	--	---	---	---	TCCCAGCCTATCGGTCAATTTGGAATATGACACTGACACTGAGTCTCTCTGGAGAAAGATCCAAACCATCAC ACAAACGGTCAGACCCAACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	---	---	---	TCTGCCTTTGGTGCAGGAGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTOCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCGCCAAACAGAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	---	---	---	AAGCATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTGTATGCCAAGGGCTTCTGTGAGGAGA
ESTD- BF882	--	--	---	---	---	TCTTTCAAGATCCGCATCTGCGCCTGTTGGGCATCGCTCCGCTAGGTGTACGCGCTCCACAGCTGG GGTGAGGGGGTGTGGTCACTGCGGGGGCGGGTGCAGACCCACGCGGGCTGGGAGGACTTCAOCC CGCTCACCTCCGTTCTCGCAGCAGTCTCCGCATCGTGACT
ESTD- ETS2	--	--	---	---	---	ACTCACAGTCTTTTAAAGTGAATAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGAACCCAGGAACAGCAATGCAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCTATTCAGAAAGTTAGTTTG
ESTD-F2	--	--	---	---	---	GATAAGTACACTGAGGCCCGCAGGAGGTTATTGCTAGTAGCCCCAACTGTGCATGCACGCTTAAOCTCT GCACCAATGGCTCCAGGCCCGCTAGGGGAAGTGGGGGATCTAGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCGCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	---	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGTCCATTTTGGTTAATATTTGTGTAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC

ESTD- G0H	--	--	--	---	---	CGCAGACCGGTCAGTGTGGGGTCGGGAGTGTGGAGGGAAGGAGGGAAGTGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTCTGCAGAGAAAGCGGGGAGAACACAGAGCAACTGGCTAA GTGTAAAGGACCTCTGTGCGACCGTGTGTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGACGTGGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTATGTCATGGCAGCTCTAATGACAGGATGGTCCGCTGCTGAGGCCACTCTCTGGTCAACATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCCCTGAGCCGAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACG TGCAGCCTAATTACTCAAAAGCTGTCCCGAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCCACAGGCATCTTG AAACCAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTCATCTGCGGTGCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	CTGGCTGCGCCGACGAGCTGTGCACTGGACCTGGACGGCGCGCCAGGCTCACTCTATAGTGGGTG TATTCGTCCACAAATGCACTCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGGAAGTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCACATCTTGGCCTTG AGGCCCTGCAGGACCCCAAGAGCCCAAGCATCCGAGGACAGTCTACTATATCTCAGATGACA CGCCTACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTCCCTTATCCCTGATGTATGGATTGGCTTCTCTGCTG
ESTD-HT2	--	--	--	---	---	GGGTAAATTTCCGAGCACTTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAGATGTTACAGTTTGTACAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCTGGAAGTTTCAAACAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAACGAGCCGCGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCTTCTATCGGCAAGAAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACAGCCGCGAAGAGTCACTGAGACTGGCAGCTTCTGACGAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACACAAGCCGAGGAGAAATGAACTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTGGTTTCTTCTCTCTATCATCTTATAGATTGATGTATGCTCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCTCCTACAAAATGAAA ACATTTCTGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCGCTCATTCACGGTCTTGGCAGGAGGTGCCCTGGGAGAGAAGGAAGATGTTT CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	--	TTTACTATTCAATGGATACAGAAATGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGGCAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACGAAAGT ATGTAAATACTTCACAAAATACTAATAACGGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	--	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTATTATTATTATTATTATTTTGTG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGCAGTGGCAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCCTGCTCAGCTCCCGAGTGTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAAATTTTGTATTTTGTAGTGTAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	--	--	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	--	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTCTGCTAAGTTTTCCTTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	--	ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	--	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATGTACCGTAGCAAAACTGCATTGGTATTAGA AAATAAAAAATTTCCAATATGTAGTGTCTGTATTACCTGCCTCTGCCATGCAGCATATAGCCTGT GGGAACCAAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	--	TACACACTTCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	--	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCCACTTCTCAGCTCTGCCCTGTCCCTGCTGCTGCA AGGTTTGTCTTAATCTCAATCAATGCTCTCTCACTTTAGCAGCTGTGGGTTTGTGTTGTTTC TCTGTTTTGCTTAGTATCTGACTACTTTTTAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAAGTTCACAAATTTATTAAAAATTTTTCACCTG
ESTD-MCC	--	--	--	--	TTGTCAGGAGTGTGCTGATGCTGCTCCCTCCCACTCTGTCCCTAGCCAACTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTGCTCTTCCAAAGGTTTGGTCAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCTCTGTTTACATGG
ESTD-NF1	--	--	--	--	ATTATCCAGATGAATTTACAAAATATACCAGATCCCAACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	--	---	---	---	---	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTCTAAAAAAGAAAAAAGAAAGAA AAATTTAAAGGTGACTTATATCCACTGCACACTGCCTAGCCCAAAACGCTTATTTGGTAGG ATCAGCCTCATTTTGTGCTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATCTGAG AAAACTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	--	--	--	---	---	---	---	---	---	TGTCCCTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NRAMP	--	--	--	---	---	---	---	---	---	GGAGGAGGAGGTGGGGGGGCTGTCTGCTCCAGGTCCACAGACCAGAGAAAGCGGCTCAGTG TATCCCCACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NRAS	--	--	--	---	---	---	---	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTATGTAGGGTGATATGGATACTTTTGTGTTGTTGATTATATTAGCAATTTGAGGG ACAAACAGATAGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTCG ATTCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	--	---	---	---	---	---	---	GTGACCTTCTCACTTTAAAAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGAGAGTATGTAAACA
ESTD-PAI1	--	--	--	---	---	---	---	---	---	GCCACCACCCACCCACCCAGCACACCTCCACCTCAGCCAGACAAGTTGTTGACACAAGAGAGCCC TCAGGGCAGACAGAGAGTCTGGACACGTGGGAGTCAGCCGTGATCATCGGAGCGCGCGGCAC ATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCAAGTCTCTAGACAGACAAAAACCTAG ACAATCAGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	---	---	---	---	CTCTTCAGGAACCCAGTCTTCTTACCAACAGACTTATGCTGCCAGAGGTACAAACCCGTAGA ACTTCTCTCACTGTAATTTAGTTAAAGGAATCGAACTGGCTCGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTCACTTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAAGCTTCACTTAGGCTTTCTGTATACCATGCC
ESTD- PBDA	--	--	--	---	---	---	---	---	---	CCTTCTCATGCCCAGATGGAAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAAATCTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-PS-1	--	--	--	---	---	---	---	---	---	GGGAGTAAACCTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGTTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACACCATAGCCTATTTCGTAGCCATTAATTTGGTTTGTGCCCTACATT ATTACTCTTGCCATTTTCAAGAAAGCATTTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTGGCACAGATTATCTTGTA
ESTD- PXMP1	--	--	--	---	---	---	---	---	---	ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAAAGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAGTCTTATGAAATTAATCTT
ESTD- Per/RDS	--	--	--	---	---	---	---	---	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGGAGGCTGGCTG CTGGAGAAAGAGCGTGGCGGAGACCTGGAAAGGCT

ESTD-RDS	..	--	--	---	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTGGAGAGAGCGTGCCGGAGAACCTGGAAGG CCTTTCTGAGAGTGTGAAGAGCTGGGCAAGGCAACAGGTGGAAGCCGAGGCGCAGACGCAGG CCAGGCCCCAGAGGCTGGCTGAGGCCCCCTGGGCCCCCTCCCTCCCAACACTGAGAAATAGTGCAC CCAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- FYRI	--	--	--	---	---	---	CTTCGTACGGGAGGTACGTCCTCCGCCCTCTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGATACCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGGAGCCACCTGGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCCTGTGGTCCGGAGCCAGGTTGTCTTCTCTGGAGCCTGAGGAGTTGTGTCTGTGTG CAGTCCCCCGGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCTTTGGCCCGGAGAAAGAC ATTTACCACTGGCCATGTCCCTGGCTGTGTGACACCCCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCCAAGCCAGTTTCTAGCAAGGCGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTACATTTGTGGATGTTTCTTTGTGTGCGAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTTGAAGAGATCTTTGCCAGTCCAATGTCTCTAGAGAG TTTTCCCAATGTTTTCTGTAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAAGTGGTACCATTTTCATAGGGCCATCAGTTCAATCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTCTTCCAGTATGGATGGGATTTATGATGGGGGG GAGAAAGCAAAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	--	--	--	---	---	---	TGCGGCCCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTGTG GCCAGAAAGACCCCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCTCCCACTTTCCAAATCCCGCCCGCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTTATCTCTCTGTGAGCTTCTGGATTTCTTGTCCCAAGCAAGAGAGTCTATGC CAAGGAGAAAGCTGTGCTTTCATGGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGATCCAGACAAAGAGGTCAATAATTGATGTGCGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

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ESTD- TYRP1	--	--	--	---	---	AGTAGTGGATGAAGCTAACCGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCAATTAGTATCACAA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACTTTATTACCTCTCTTCT AATACAGCATATGTTAGAATTAAAGTTCTAGGCATACCT
ESTD- VB12	--	--	--	---	---	TTCCAAAGGCTCAATACAAGCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAGGTCACAGACAGGAACACCCAGTG ACTCTGAGATGTCACACAGACTGAGAACCACCGTTATATGACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	--	---	---	AGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTCCACACTGTCCTTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTGCTGCAGGATGTG CGACGTGTCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTAATACGGAATTACTAAGGACGACACAGAGGCTTAATTGAAAA TATCCCAAGTTGAAATGTCTCAGTCTGCTGTGGGTAGATGCAGGATTTATATGATCCGTTAACCC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCCAAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	--	---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCACTACCCCTTTGGTGGCTACAAGATGTGG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAAACCTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCCTCTATTGCCCCAGCCCCAGGACAGAGCTGATCCTTGAACCTCTTAAGTTCACATTGCCAGGA CCAGTGAGCAAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCCCGG GTCACTC
EST51976 7	--	--	--	---	---	AGGCAGAACTGGGCCCCCATCGGGGGGACGTGGAAAGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTCTTCAGCACTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGAGGAGGTCAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCTGGTGC

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EST11458 6	--	--	--	---	---	CCACCTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCAGATGATTTACCATTTTCCACAGTGGT CCATTAAAAACATTCTATGAGCCAGGAGAGATTACGTATTCTGCAAGCCGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGCTTCCTCCAGGTATTGTCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGAAAAAGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGAACCTGGTCTCTTGCCATTGCGGCCCTCTGCGGCCCTCTGCGGCCGTGG TCCTCTGGTGTGCTGGTGTGCTGGTCAACGGTCTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGAAACGATGGTCCGCCAGGTGCGGATGGTCAACCCGGACACAAGGAGAGCGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCATTTACAGGGCTCTAATGATGTTGAACTTGTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTGTAGATGGTCTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGTTTACTCTCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCCGATGGGTGAGAACTGTTCTGTCCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACCTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGAAGTCCT GCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACAAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAAGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGTTTCAGTTACTTATGAATATTATGATACCTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCCTTTTATGGACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGCTACTA TAGTCCAAAGTGAA

EST10398 2									TGCTGGGTGGCAAGGCTGCAAAACAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTTACATTTGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTCCTCGGGCCAAGAGTATCTACCAATAGTGTCTATTAGGCAATTTG
EST36751 7									CCAAGTCGTTCAATTTAGCTTTCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562									CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAAACTTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCAATTAATAACAAATATTTACCTTTTGAAAAAATAAATG AAGGATTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCCCTGACGTTTTTGAACAATACAGAT GCCTTCCCTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3									GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTACAGGATGGAAGACTGGCTGCTCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTTCACACCTACGTCCACTTCCAAGTAAGGCAAACTCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3									TTCCGCCAGCCCCCATCCTTGGCACCTGGTCCCTCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTCGGTAACATCGGGCGGGCGGCTCCTTGAGCATAGCTGGACCGTTTCCGTATAGGAGG ACCGGTAGGCTTCTGTCCCGGGCTTGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACAGTG
EST58707 7									CAGTGATCTGGAAGCCTACAGGACACCAAAATACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTACGATCTTTGGCTACATGAAGCCAAATTCGAGAGACCTTAGAAGATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAATTCACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6									AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGCGCGCAGGCCCGGCTGGCGCGGACATGGAGGA CGTCCGGCGCGCTGGTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGAGC TGCGGGTGGCGCTCGCTCCACCTGGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8									CGCTGTGCAGTACCGCGGAGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCCTCCACCTCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGC TGGCAGTGTACAGGCGGGCGCGAGGGCGCGAGCGGCTCAGCGCCATCCGCGAGCGCGCTG GGGCGCTGTGGAACAGGGCGCGGTGGGGCGCGCCTGTTGGGCTC
EST36770 4									TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGCTGGGCTGACCAAAATATACTGGTTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAAAGGCCCTAAAGAGGCTTATG

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EST26021 1	..	--	---	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCTCTGCAGCACTTCACCTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTTCTTTTGAACAAGACAAAGCAAGCC
EST51212 0	--	--	---	---	---	ATCCTGAGCTCGCCATAAGCTTCITGGTTCTACTTCTCTCTCCACAAGCCCCAATTCACCTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	---	---	---	GTCCGAATCCTCCTCTGAAAGTGCCGGTTAATCTGCTCATGACGCTGCGGCTGTTGTCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGGTTAGGACGCGGTCTCTGCGTGATCCTAAGCTCT GAGAGCAAACCTCCCTTGAAGCTGGAGTGGGGTTAGGGACGCGGGTCTCTGCGTGATCCTAAGCT CTGAGA
EST53018 6	--	--	---	---	---	ACAATCCAGGTACACATTCACAGAAGAGGAGGGTGGTCAGTAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	---	---	---	CTTCCTATGGGATTGACTTTATTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAGA GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGCACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2	--	--	---	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCACAGAGACCGGCTCAAGG ATCCCAAGGCCCAACTCCCGAACCACTCAGGGTCTCTGTGGACAGCTCACTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	---	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAACCCCTCTTCTCTTCTCCCTTGGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGACCCCAAGAAAT CACAGGTGGGCACGTGCGCTTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082 0	--	--	---	---	---	TCAGGGTGGCTGGACCCCAAGCCCAAGCTCTGCAGCAGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGTGAGCCCAAGGGGCCCCAAGGCAGGGCACTGGCTTCAGCTGCTCAGCCCTGCTGCTGTCAC CCAGATCACTGTCTTCTGOCATGGCCCTGTGGATGCGCCCTCTGCCCCCTGCTGGGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGG
EST45311 0	--	--	---	---	---	GGCCTCTCTCTTCCAAATCTGTCCCTATAGTTTCTCTATTAAGTGAACATACATGCTCTTTTAGT GGATAGATGCACACAACACACAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTTATTCATGCGCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

EST65258 8	--	--	---	---	---	TGCCCCATCAGCGCGGAGACATGGCTTGCCACAGCTCTGAGGATGTCCACCAATTAACCAAAAT CCAGTTATTTCCACCCTCAAATGACAGCCATGGCGCGGGTCTCTGGGGCTCGTGGGGGG ACAGCTCCACTCTGACTGGCAGCTCTTGATGGAGACTTGAGGAGGAGGCTTGAGGTTGGTGAG GTTAGGTGGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	--	--	---	---	---	ATGCAGGATGAAGGTGGACAGGAGGAGAGGCGCAACCTGTATCCAGGGCTGCAGATGTCGCTG GACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	--	---	---	---	ATACTAGTACAAAGTGGTAATTTTGTACATTACACTAAATTAAGCATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAATGCTTATTTAAATGACAGTGGAAG TTTTTTTCTCGAAGTCCAGTATCCAGAGTTTGGTTTTTGAACCTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGCTGGGGTTTTTGGTGCATGCA
EST35879 9	--	--	---	---	---	GAGATCGGTGTGAGTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGCGCTCCACCGATG GAACTGCCGGCAAATCTGACAGGTGTGACCCAGGCTGTACCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCCTGGATGAA
EST68308 5	--	--	---	---	---	GGAAGAGATTTAAGAAGCTTGATTGGACAATCTGTTCTTTGAGTGTGGAAGATTGATGTCTCT GCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAACTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST54045 6	--	--	---	---	---	GGAATATTAATAATTTTAAATACCTCCAATTTGCTTATCTCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTGATGTTGGCAATTTGTTTCTACAAAATCGGATGGGAATCT GTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTTGACTTTTATCAT
EST52908 0	--	--	---	---	---	ATCACAGGTCTCTGGTCTCTGCCATCATTTCTCTGGGAGAGATGGATGGTCTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST19590	--	--	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAATGAC
EST76136	--	--	---	---	---	TGAAGCTTCTGCCCAGCTTGCAATGTTTCTAGGAGAACCCGGTCTATACCTTTATCTATAGCCTTCCCG TAGGTCTT
EST58607 0	--	--	---	---	---	CTCTGGATGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCTGTAGTCATCATAGTTGTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAAAGGACAGCCACATGGCGGGGATGGCCGGGAGTCTGGT TGCGGCACGGCTGTGCCCTGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCATAAACCTTTGTTTCT TGGCCAAGGAGGGGGGTGCCATGCTGAGATGATGAGTGGCGCC
Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence						

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
- 5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.